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Estimates of a Biologically-Based Spawning Goal and Biological Benchmarks for the Canadian-Origin Taku River Coho Stock Aggregate

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Foreword

This series documents the scientific basis for the evaluation of aquatic resources and ecosystems in Canada. As such, it addresses the issues of the day in the time frames required and the documents it contains are not intended as definitive statements on the subjects addressed but rather as progress reports on ongoing investigations.

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ABSTRACT

This paper establishes a biological frame of reference for spawner abundances of the Coho Salmon (*Oncorhynchus kisutch*) stock aggregate originating in the Taku River in northwestern British Columbia. This transboundary stock aggregate is managed cooperatively by Canada and the US under the Pacific Salmon Treaty.

The project focused on fitting alternative Spawner-Recruit (SR) models and estimating biological benchmarks for each model. A long time series of good-quality data are available for Taku River Coho Salmon at the aggregate level including: spawner estimates based on a consistent mark-recapture survey covering the period 1987-2013; recruitment estimates for the 1987 to 2009 brood years based on catch and escapement data and coded-wire tag recoveries in Alaskan and Canadian fisheries and surveys; and annual age and sex composition estimates.

Estimates of biological benchmarks for the Taku River Coho Salmon aggregate were robust to alternative assumptions. For example, estimates of the number of spawners that maximizes sustainable yield under long-term average conditions (S_{MSY}) are remarkably consistent across 3 variations of the Ricker SR model for the base-case data set and all available years of data (1987 -2009 brood years). Median estimates range from 62,000 to 79,000 spawners, differing by less than 30% from each other. Based on statistical and practical considerations, the DFO's regional peer review process recommended one of the model-data combinations as the most appropriate basis for advice regarding management goals for Taku River Coho Salmon: the Ricker AR1 model, which corrects for observed time-series patterns in residuals, fitted to estimates of total spawners and total adult recruits based on the age composition in the Canyon Island survey.

In addition, we present various reference points derived from the SR model fits to address policy considerations under Canada's Wild Salmon Policy (e.g. upper and lower benchmarks for the relative abundance metric in a status assessment) and Alaska's Sustainable Salmon Policy (e.g. range of spawner abundance with given probability of achieving some specified proportion of maximum sustainable yield).

As a consistency check, we also used 2 methods recently applied in data-poor settings: one based on percentiles of observed spawner abundance; and the other based on average smolt abundance observed for large brood years. These are more widely applicable and account for the majority of spawning goals for Pacific Salmon currently in use by DFO and ADFG. The percentile method produced a cautionary approximation of S_{MSY}, but the smolt capacity method was highly sensitive to the productivity assumption, giving approximate S_{MSY} estimates that were either much higher or much lower than the SR-based estimates.

Estimations d'un objectif de frai fondé sur des données biologiques et points de référence biologiques pour l'ensemble des stocks de saumons coho d'origine canadienne de la rivière Taku

RÉSUMÉ

Ce document établit un cadre de référence biologique pour l'abondance des reproducteurs dans l'ensemble des stocks de saumons coho (*Oncorhynchus kisutch*) provenant de la rivière Taku dans le nord-ouest de la Colombie-Britannique. Cet ensemble de stocks transfrontalier est géré en collaboration par le Canada et les États-Unis dans le cadre du Traité sur le saumon du Pacifique.

Le projet visait à ajuster des modèles reproducteurs-recrues (RR) différents et à estimer les points de référence biologiques pour chaque modèle. Une longue série chronologique de données existe sur les saumons coho de la rivière Taku, y compris des estimations du nombre de reproducteurs basées sur un relevé de marquage et recapture uniforme s'étendant de 1987 à 2013, des estimations du recrutement pour les années d'éclosion de 1987 à 2009 reposant sur la récupération des micromarques magnétisées codées dans les pêches et relevés alaskiens et canadiens ainsi que des estimations annuelles de la composition selon l'âge et le sexe.

Les estimations des points de références biologiques pour les saumons coho de la rivière Taku ont résisté aux hypothèses différentes. Par exemple, les estimations du nombre de reproducteurs soutenant un rendement maximal (R_{RMS}) constant à long terme dans des conditions moyennes sont remarquablement constantes dans les trois variations des modèles RR de Ricker pour l'ensemble de données de référence et toutes les années où des données sont disponibles (années d'éclosion de 1987 à 2009). Les estimations médianes varient de 62 000 à 79 000 reproducteurs et diffèrent de moins de 30 % les unes par rapport aux autres. Le processus d'examen régional par les pairs du MPO a permis de recommander, d'après des statistiques et pratiques, l'une des combinaisons de modèles et de données comme élément de base le plus adéquat pour formuler des conseils à propos des objectifs de gestion concernant le saumon coho de la rivière Taku. Il s'agit du modèle de Ricker AR1, adapté aux estimations du nombre total de reproducteurs et du nombre total de recrues sur la base de la composition selon l'âge du relevé réalisé à Canyon Island. Ce modèle corrige les régularités temporelles observées dans la variance résiduelle.

En outre, nous présentons divers points de référence tirés des ajustements du modèle RR afin d'aborder les considérations stratégiques de la Politique concernant le saumon sauvage du Canada (p. ex., points de référence supérieur et inférieur du paramètre d'abondance relative dans une évaluation de la situation) et de la *Sustainable Salmon Policy* de l'Alaska (p. ex., plage de l'abondance des reproducteurs et probabilité donnée d'atteindre une proportion précise du rendement maximal soutenu).

Pour vérifier la cohérence, nous avons également utilisé deux méthodes récemment appliquées dans des situations où l'on dispose de peu de données : une fondée sur les centiles de l'abondance des reproducteurs observée, et une autre fondée sur l'abondance moyenne des saumoneaux observés lors des grandes années d'éclosion. Ces méthodes peuvent être appliquées à plus vaste échelle et tiennent compte de la majorité des objectifs de frai pour le saumon du Pacifique actuellement utilisés par le MPO et le Alaska Department of Fish and Game. La méthode fondée sur les centiles a produit une approximation de précaution de la valeur de R_{RMs}, mais la méthode fondée sur la capacité en saumoneaux était très vulnérable à l'hypothèse de productivité étant donné les estimations approximatives de R_{RMs} qui étaient soit beaucoup plus, soit beaucoup moins élevées que les estimations fondées sur le modèle RR.

1. INTRODUCTION

1.1. SCOPE OF HIS PAPER

1.1.1. Purpose

The purpose of this paper is to establish a biological frame of reference for spawner abundances of the Taku River Coho Salmon (*Oncorhynchus kisutch*) stock aggregate (step 1), which can then be used to evaluate status and set management goals (step 2). This paper focuses on the first step, but includes a discussion of implications for the second step.

The specific objectives of this work are to:

- Review production, escapement and smolt abundance data for Coho Salmon originating in the Taku River upstream of the Canada-US border;
- Develop biological benchmarks at the aggregate level including the number of spawning adults that would produce a maximum sustainable yield of Coho Salmon using various models;
- Examine and identify uncertainties in the data and methods;
- Comment on future data needs and considerations which could allow development of biological benchmarks at the Conservation Unit level.

These tasks primarily emerged from an obligation in the current Transboundary Chapter of Annex IV of the Pacific Salmon Treaty (PST) to… *"develop a joint technical report and submit it through the various Parties review mechanisms with the aim of identifying and establishing a bilaterally agreed to MSY goal for Taku coho"*. It was agreed by the Transboundary Panel of the Pacific Salmon Commission (PSC) that Canada would take the lead on addressing this obligation.

1.1.2. Analytical Approach

Canadian-origin Taku River Coho Salmon are a transboundary stock managed cooperatively by Canada and the US under the PST. Therefore, this analysis is set up to cover the range of approaches applied in recent work published by Fisheries & Oceans Canada (DFO) and the Alaska Department of Fish & Game (ADFG).

In this paper, we compare the results from alternative approaches recently applied in similar reports (Section 1.3), provide science advice for interpreting the results, and discuss implications for using the results.

We apply 3 alternative approaches to establish a reference range for spawner abundance of the Taku River Coho Salmon aggregate:

- *Percentile Method:* Based on some percentiles of observed spawner abundance. ADFG has a step-wise algorithm based on contrast in the data (e.g. Table on p6 of Volk et al. 2009), while DFO has used 25th and 75th percentiles as the default (English et al. 2014). Both implementations refer back to Bue and Hasbrouck[1] and label the resulting range a Sustainable Escapement Goal (SEG);

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[1] Bue, B.G. and J.J. Hasbrouck. (Unpublished). Escapement goal review of salmon stocks of Upper Cook Inlet. Alaska Department of Fish and Game, Report to the Alaska Board of Fisheries, November 2001 (and February 2002), Anchorage.

- *Smolt Capacity Method*: Based on average smolt abundance observed for large brood years, divided by regional average for smolt per spawner at S_{MSY} (e.g. Shaul & Tydingco 2006);
- *SR Model Method*: Based on fitting spawner-recruit (SR) models and estimating biological benchmarks for each model (S_{MSY}, S_{MAX}, S_{GEN}, S_{EQ}, see Sec 1.3.2). Two estimation approaches can be used for this:
    - Maximum Likelihood Estimate (MLE) estimate with bootstrap intervals (e.g. McPherson et al. 2010, Holt and Ogden 2013)
    - Bayesian estimates using Markov Chain Monte Carlo (e.g. production model of Eggers and Bernard 2011, Grant et al. 2011, Holt and Ogden 2013);

Alternative SR models, fitted to either adult recruits per spawner or smolts per spawner, include:

- *Ricker*: characterized by a density-dependent drop in recruitment at larger spawner abundances;
- *Ricker AR1*: Ricker with a 1-year autoregression term to correct for patterns over time (i.e. good years tend to follow good years, so that residuals are not independent);
- *Ricker – Kalman*: Ricker with Kalman filter which allows for changing productivity over time and explicitly estimates the pattern in the productivity parameter (Peterman et al. 2000, Peterman et al. 2003, Dorner et al. 2008).

We explore whether results are robust by:

- Using alternative data assumptions:
    a) alternative age composition data sets resulting in alternative estimates of adult recruits by brood year;
    b) total spawners or female spawners;
- Evaluating different time windows (i.e. retrospective evaluation);
- Dropping individual data points (i.e. jackknife evaluation).

Note that the project focused on fitting alternative Spawner-Recruit (SR) models and estimating biological benchmarks for each model, because long time series of good-quality data are available for Taku River Coho Salmon at the aggregate level. We also present results for the data-poor approaches as a consistency check, because they are more widely applicable and account for the majority of spawning goals for Pacific Salmon currently in use by DFO and ADFG.

1.2. TAKU RIVER COHO SALMON

This overview is based on two reports compiled by the Taku Fish Sustainability Working Group (TFSWG 2003a, TFSWG 2003b) and the Integrated Fisheries Management Plan for Transboundary Rivers Salmon (DFO 2014).

1.2.1. Brief Overview of the Taku River Watershed

The Taku River is a large transboundary river in northwestern British Columbia. Approximately 90% of the 19,000 km^2 drainage area lies within B.C.; the remainder is located in Alaska, including the mouth of the river about 45 km north-east of Juneau. Appendix A includes a map of the Taku River drainage.

The drainage spans two main ecoregions: the Boundary Ranges ecoregion characterized by rugged mountains, ice fields and glaciers and moist climate strongly influenced by its proximity to the ocean; and the drier sub-Arctic climes of the Yukon-Stikine Highlands Ecoregion.

The drainage is ecologically and physiographically diverse characterized by three dominant aquatic regions, based primarily on geomorphological features: (1) the dynamic, highly braided and glacially influenced streams and Taku mainstem in the lower river; (2) the lake dominated and glacially influenced streams on the eastern slopes of the Boundary Ranges; and (3) the high elevation streams and small lakes of the Stikine Plateau. These 3 regions are further divided into 5 distinct watershed units, each with unique biophysical features and resulting differences in salmon distribution: Lower Taku, Nakina, Nahlin, Sheslay, and Inklin.

The lower Taku River is highly braided, confined within a wide mountainous valley with major glacial influences in close proximity to the mouth (e.g. Tulsequah Glacier and its unique jökulhlaup or sudden release of glacially impounded melt-water). This is sharply contrasted by the small lakes and streams surrounded by boreal forests and uplands of the Stikine Highlands. Transition zones between the ecosystems are characterized by high gradient watercourses and deep canyons (e.g. Nakina River canyon).

Amongst the large transboundary rivers (Alsek, Stikine, Taku), the Taku River is a major contributor of Chinook, Sockeye, Coho, Pink and Chum salmon and steelhead with most of the spawning areas located in the Canadian portion of the drainage. Salmon distribution is widespread throughout the Inklin River and its tributaries, whereas velocity barriers in the Nakina River drainage prevent Salmon from accessing a greater proportion of the larger headwater lakes and streams, such as Sloko and Nakina lakes.

1.2.2. Population Structure of Taku River Coho Salmon

The Taku River is the largest producer of Coho Salmon among the transboundary rivers, with a median aggregate total run size of 177,000 adults and ranging from 51,000 to 340,000 fish since 1990.

Coho Salmon spawning areas in the Taku River watershed are widely distributed. Notable spawning locations include: mainstem Taku River, Nakina River, Hackett River, Nahlin River, Tatsatua Creek, Kowatua Creek, Tulsequah River, Sloko River, and streams located in the U.S. section of the Taku River (Appendix Figure A 1).

Returning adult Taku River Coho Salmon generally reach the river mouth and cross the Canada-US border in mid-July with the peak of the run arriving in early to mid-September. For international cooperative management and harvest sharing purposes, two run components are considered separately: the early part of the run (coho salmon that migrate prior to statistical week 34, roughly mid-August); and the late run (coho salmon that migrate into the river after statistical week 33). The late run is subject to specific harvest sharing objectives outlined in Chapter 1 of Annex IV of the PST.

Under Canada's Wild Salmon Policy (WSP), one Coho Salmon Conservation Unit (CU) was initially identified for the Taku River based on ecotypic characteristics (Table 26 of Holtby and Ciruna 2007). However, subsequent unpublished work by Holtby and others has identified three potential CUs (TAKU-early timing, TAKU-mid-timing, and TAKU- late timing) based on run timing information and three main aquatic sub-ecotypes in the drainage as described above. Timing of upper Inklin populations (e.g. Hackett River) is believed to be early; the mid-timing populations of the eastern slopes of the Boundary Ranges include, for example, Coho Salmon spawning in the Kowatua River (little Trapper Lake). Coho Salmon that spawn in the mainstem Taku and side sloughs constitute late-timing populations.

1.2.3. Fisheries Harvesting Taku River Coho Salmon

Three fisheries target salmon in the Canadian section of the Taku River: the Taku River Tlingit First Nation food, social and ceremonial (FSC) fishery, the recreational fishery and the commercial gillnet fishery. The commercial fishery and most of the FSC effort utilizes gillnets set from outboard-driven riverboats in the lower river just upstream of the Canada-U.S. border. The Canadian fisheries and management processes are described in the annual Integrated Fisheries Management Plan (IFMP), the most recent of which is the *Integrated Fisheries Management Plan for Transboundary Rivers* (DFO 2014).

Fisheries in Alaska that also target Taku salmon stocks include the District 111 commercial drift gillnet fishery in Taku Inlet, the Juneau area sport fishery, and a limited personal use fishery in the lower Taku River in Alaska. S.E. Alaskan troll fishers also catch Taku salmon stocks in multi-stock fisheries which generally focus on Chinook and Coho Salmon. Seine fisheries conducted along the migration routes also may encounter Taku stocks, notably Sockeye and Pink Salmon.

Appendix A includes a summary of the catch of Taku River Coho by fishery. Median exploitation rate (ER) since 1990 is 49%, with most of the harvest (approximately 89%) taken by the US primarily in marine troll, gillnet and recreational fisheries; the remainder is harvested in small in-river fisheries in Canada.

Cooperative and coordinated management regimes for Taku Chinook, Sockeye and Coho Salmon have been developed by the Transboundary Panel of the PST pursuant to arrangements contained in current PST, Annex IV, Chapter 1, which cover the 2009-2018 period. Salmon stocks returning to the Taku River drainage are cooperatively managed and assessed by DFO and the Alaska Department of Fish and Game (ADFG) through the Canada/U.S. Transboundary Technical Committee of the Transboundary Rivers Panel (pursuant to the PSC). Under provisions of the PST, Taku River Coho Salmon are managed as an aggregate. Annual management plans, catch data, and spawner data are documented in technical reports prepared by the Transboundary Technical Committee (e.g. PSC JTTC 2014, PSC JTTC 2012)

The development of the IFMP, which includes decision guidelines and specific fishery management plans for Taku River fisheries in Canada, involves consultation with the Taku River Salmon Management Advisory Committee (TRSMAC) and the Taku River Tlingit First Nation (TRTFN). Recommendations of the Transboundary Rivers Panel (TRP) of the PSC provide an overarching back-drop for these decision guidelines as do DFO policies, scientific advice and the experience of fishery managers.

The *Integrated Fisheries Management Plan* (DFO 2014) includes abundance-based trigger points for Canadian harvest measures, but no similar management reference points specific to Taku River Coho Salmon are in place for the Alaskan fisheries which harvest larger aggregates and account for the bulk of the total ER of Taku River Coho Salmon. As a result, total ER is driven by other factors such as abundance of other species and stocks, weather, water levels, and price.

1.3. BENCHMARKS FOR PACIFIC SALMON

1.3.1. Frames of Reference

Taku River Coho Salmon are managed cooperatively by Canada and the US under the Pacific Salmon Treaty. The two agencies responsible for salmon management operate under similar policy frameworks and recent work related to biological benchmarks is conceptually consistent.

However, there are important differences in both methodological details and subsequent use of the results.

This section focuses on conceptual differences, which we characterize as *frames of reference* (i.e. the yard stick being applied to biological information) but we note analytical differences at the end of Section 1.3.5.

Two institutional frames of reference have emerged for Pacific Salmon in BC and Alaska. Both relate back to a common biological frame of reference, but they differ in how the biological information is used.

1.3.2. Biological Parameters

The biological frame of reference has been widely used across jurisdictions for over 60 years (e.g. Ricker 1954), with well-documented theoretical basis (e.g. Walters and Hilborn 1992, Quinn and Deriso 1999), and rapid evolution of methods as computing power increased and shifted implementation from mathematical solutions to ever more computing-intensive approaches like bootstrapping and Markov-Chain Monte Carlo (MCMC) to capture uncertainty (Pitcher 1999, Megrey and Moksness 2008)

The fundamental step is to fit a biological production model (e.g. linking spawners to adult recruits) and estimate population parameters like productivity and capacity based on the shape of the model. Biological benchmarks (Table 1) can then be directly calculated from the fitted model shape. These benchmarks have widely accepted technical definitions and can be calculated independently of any management considerations. For example S_{MSY} is always defined as the spawner abundance that maximizes sustainable yield over the long-term (i.e. the point with the largest difference between spawner abundance and subsequent recruits), no matter how the stock is managed (e.g. fixed escapement vs. fixed ER).

The following two sections outline how this biological information is used by two different agencies to determine management goals and evaluate status.

1.3.3. Alaska's Sustainable Salmon Policy (SSP)

Two relevant policies were formally adopted by the Alaska Board of Fisheries (Brannian et al. 2006): the *Policy for the Management of Sustainable Salmon Fisheries* (Sustainable Salmon Policy; Alaska Administrative Code: 5 AAC 39.222) and the *Policy for Statewide Salmon Escapement Goals* (Escapement Goal Policy, 5 AAC 39.223). Brannian et al. (2006) and Volk et al. (2009) summarize the concepts and definitions. Clark et al. (2009) illustrate the practical implications using case studies.

These policies require that spawning goals be identified for all stocks and reviewed regularly. The policies also establish criteria to consider in setting spawning goals and outline the development process. They identify four types of spawning goals:

- *Biological Escapement* Goal (BEG): Based on the estimated range of S_{MSY}, where sufficient data is available.
- *Sustainable Escapement Goal* (SEG): Based on observed range of spawner abundances.
- *Sustained Escapement Threshold* (SET): Level where sustainability is jeopardized, set below the lower end of BEG and lower end of SEG.
- *Optimal Escapement Goal* (OEG): Range chosen based on biological, harvest, and allocation considerations. This may differ from the BEG, but must be above the SET, and requires a documented justification including effects on expected yield. OEGs are set by

the Board of Fisheries based on a review of BEG, SEG, and SET determined by ADFG (Alaska Administrative Code: 5 AAC 39.222).

The resulting escapement goals are used to bound three regions of concern.

- *Yield Concern*: results from a chronic inability to maintain yields or harvestable surplus above escapement needs
- *Management Concern*: results from a chronic inability to maintain escapements within the bounds of a BEG, SEG, or OEG.
- *Conservation Concern*: results from a chronic inability to maintain escapements above an SET.

Chronic inability is defined as "continuing or anticipated inability to meet escapement goals over 4-5 year period (generation time of most species) despite use of specific management measures".

Several large-scale reviews of escapement goals have been completed since the SSP was formally adopted (e.g. Brannian et al. 2006, Volk et al. 2009)

Note that the definition of yield concern relates to potential harvest rather than actual harvest. Specifically, a yield concern arises if spawning goals are being met, but there is no harvestable surplus available (e.g. when managing to a long-term average S_{MSY} goal during a period of reduced productivity). This is not the same as concerns over foregone yield or potential future declines in productivity associated with large spawner abundances (i.e. over-escapement). These latter considerations are implicit in setting spawning goals at S_{MSY} (i.e. in the BEG), but are not formally defined in the SSP and may be outweighed by other consideration when choosing an OEG).

1.3.4. Canada's Wild Salmon Policy (WSP)

After a long development and consultation process (Irvine 2009), DFO released *Canada's Policy for Conservation of Wild Salmon* (Wild Salmon Policy, WSP) in 2005 (DFO 2005). The policy identifies 6 strategies and outlines actions steps for implementing each strategy. The strategies can be summarized as:

1. determine population status;
2. determine habitat status;
3. incorporate ecosystem considerations;
4. establish collaborative strategic planning processes;
5. include outcomes from 1-4 in annual implementation; and
6. regularly review performance.

Strategy 1, which describes the requirements for standardized monitoring of wild salmon status is the most relevant to the work presented here on biological benchmarks for Taku River Coho Salmon. It has three action steps:

1. Identify conservation units (CUs);
2. develop criteria to assess CUs and identify benchmarks to represent biological status;
3. monitor and assess status of CUs.

Substantial work has been completed on all three steps.

Holtby and Ciruna (2007) developed a framework for identifying CUs and presented an initial list of 420 CUs covering all five salmon species in BC. Subsequent unpublished analyses by Holtby and others applied the same approach to identify CUs in the Yukon and Northwest territories. DFO (2009) summarizes the framework. The CU delineations have since been revised as data are compiled and verified for the status assessments, but no updated master list of coastwide CUs has been formally published at this time. Taku River Coho Salmon are an example of this, because they were initially grouped into a single CU (Table 26 of Holtby and Ciruna 2007) but subsequent unpublished work may lead to future splitting into 2-3 distinct CUs.

Holt et al. (2009) developed a framework for status assessment based on a suite of metrics (e.g. relative abundance, short-term and long-term trends in abundance), as well as upper and lower benchmarks for each metric to identify three status zones (Red/Amber/Green). For the relative abundance metric, the upper benchmark is set at 80% of S_{MSY}, and the lower benchmark at S_{GEN}, the spawner abundance which allows rebuilding to S_{MSY} in 1 generation in the absence of fishing (i.e. high probability that total adult recruits meet or exceed S_{MSY}).

Holt (2009) documents the analyses behind the choice of benchmarks. Holt and Bradford (2011) further explore the properties of alternative biological benchmarks. Holt and Ogden (2013) introduce a software package for calculating the benchmarks and resulting values of the different status metrics.

Grant et al. (2011) and Brown et al.[2] compiled available data for a large number of CUs and presented WSP status metrics, which were evaluated in subsequent expert workshops (Grant and Pestal 2012, Brown et al.[3]).

Key concepts emerging from this body of work are:

- Assessments under the WSP focus on biological status. Yield considerations are explicitly excluded from this step, but are part of integrated planning under Strategy 4.
- No single metric can reflect the many different aspects of status that are considered by experts, so status integration has been done in a large workshop format (Grant and Pestal 2012, Brown et al.[3]).
- Status benchmarks are fundamentally different from management reference points (e.g. Chaput et al. 2012, Holt and Irvine 2013), but the management system can choose to set them at the same value (e.g. fixed escapement policy with goal set to S_{MSY}).

1.3.5. Comparing the 3 Frames of Reference

This section briefly summarizes our interpretation of how Alaska's SSP and Canada's WSP line up conceptually and in terms of recent implementation. In Section 5.4 we outline a proposed process to formally reconcile the two frames of reference for the management of transboundary stocks.

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[2] Brown, G.S., S.J. Baillie, R.E. Bailey, J.R. Candy, C.A. Holt, C.K. Parken, G.P. Pestal, M.E. Thiess, and D.M. Willis. 2014. Pre-COSEWIC review of southern British Columbia Chinook salmon (*Oncorhynchus tshawytscha*) conservation units, Part II: Data, analysis and synthesis. Unpublished DFO Canadian Science Advisory Secretariat working paper.

[3] Brown, G., M.E. Thiess, G. Pestal, C.A. Holt, and B. Patten. 2014. Integrated biological status assessments under the Wild Salmon Policy using standardized metrics and expert judgement: southern British Columbia Chinook Salmon (*Oncorhynchus tshawytscha*) Conservation Units. Unpublished DFO Canadian Science Advisory Secretariat working paper.

The terminology roughly matches up as follows:

- Alaska's Optimal Escapement Goals (OEG) are equivalent to Canada's Management Reference Points (MRP), because both incorporate socio-economic considerations and recognize practical constraints on implementation. The difference is that MRP could also be specified in terms of exploitation rate or run size. The development process differs between the two jurisdictions, with OEG determined by the Alaska Board of Fisheries and MRP set by DFO as part of the annual *Integrated Fisheries Management Plan* after public consultation.
- Alaska's Sustainable Escapement Goals (SEG) are equivalent to Canada's Interim Management Escapement Goals (IMEG), because both are based on percentiles of the observed spawner abundance.
- Alaska's Sustained Escapement Threshold (SET) has a similar intention as Canada's S_{GEN}, because both are designed to flag serious conservation concerns. The difference is that S_{GEN} has a formal quantitative definition and has been tested for robustness (Holt 2009, Holt & Bradford 2011), whereas the specific choice and justification of SET is left open for each specific case.

Both agencies have delineated spawner abundance ranges based on biological benchmarks, and in both cases S_{MSY} serves as the anchor point. However, interpretation differs substantially (Table 2). Under Alaska's SSP, S_{MSY} is the biological escapement goal and starting point for choosing an OEG once a BEG has been developed. Under Canada's WSP, S_{MSY} is used to delineate 3 status zones (Green > 80% S_{MSY}, Red < S_{gen}, Amber in between) for one of several status indicators used in an integrated assessment. Canada's WSP does specify how management goals should be set in relation to S_{MSY} or the 3 status zones, because status assessments look back at observed patterns, and harvest rules are designed around plausible future scenarios.

Due to these differences in policy frameworks, recent implementation by the two agencies has diverged. Table 3 summarizes high-level differences. The rest of this section compares some recent ADFG and DFO reports which differed in terms of conceptual approach, definitions, and computational methods depending on available data and policy setting.

Key differences are:

- Recent ADFG analyses have yield profiles as a standard part of the results (e.g. Fleishman and Evenson 2010, McPherson et al. 2010, Eggers and Bernard 2011, Fair et al. 2011), but yield-related information was not part of the WSP case studies for Fraser Sockeye and Southern BC Chinook, which focused on metrics of biological status, including lower and upper benchmarks for *Relative Abundance* (Grant et al 2011, Grant and Pestal 2012, Brown et al.[2], Brown et al.[3]);
- ADFG analyses commonly use a modified form of the Ricker model that accounts for autocorrelation in the residuals (Fleishman and Evenson 2010, Eggers and Bernard 2011, Fleishman et al. 2011, Hamazaki et al. 2012), but this is not used in DFO reports, except for the theoretical explorations in Holt (2009);
- ADFG analyses typically apply a bias correction before calculating biological benchmarks (e.g. Bernard et al. 2000, McPherson et al. 2010, Fleishman and Evenson 2010, Eggers and Bernard 2011, Fleishman et al. 2011, Hamazaki et al. 2012), but this has not been applied for the WSP benchmarks (Grant et al. 2011, Brown et al.2) and is not part of the WSP Software toolkit (Holt and Ogden 2013);

- Several of the reports from both agencies use simple linear regressions with bootstrap. In some cases this is the only estimation method (e.g. Bernard et al. 2000, Tompkins et al. 2005, Fair et al. 2011), but others use them side-by-side with Markov Chain Monte Carlo (MCMC) to explore the robustness of results (e.g. McPherson et al. 2010, Holt and Ogden 2013).

In each case the chosen approach depended on available data and the institutional frame of reference. The analysis for this paper was shaped by three considerations:

1. Where methods diverged (e.g. bias correction), we chose the approach taken for other transboundary stocks as the base case (i.e. McPherson et al. 2010 for Taku Chinook, Bernard et al. 2000 for Stikine Chinook, Eggers and Bernard 2011 for Alsek Sockeye, Bernard and Jones 2010 for Alsek Chinook)
2. Given the transboundary management system for Taku coho, we presented the information required by both agencies for their individual and joint planning processes.
3. Even though sufficient information for more sophisticated analyses such as spawner-recruit modeling is available, we chose to also apply the alternative approaches used for data-poor systems (e.g. of Volk et al. 2009, English et al. 2014) and to check whether the results are roughly consistent.

2. METHODS

Note: Our analyses focus on spawner-recruit models and biological benchmarks derived from the model fits, but include as a consistency check some methods used in data-poor systems. We present the methods in a progression of increasing data requirements and analytical complexity.

2.1. DATA

2.1.1. Data Sources

Consistent estimates of total run, spawner abundance, age composition, and adult recruitment by brood year are available at the aggregate level since 1987. Consistent estimates of aggregate smolt abundance and age composition are available since 1990. This section briefly describes the data sources for Taku River Coho Salmon. Section 2.1.2 summarizes the observed patterns. Tables in Appendix A list all the values.

Williams and Jones (2014) describe the survey methods for Taku River Coho Salmon as well as the analytical models used to estimate population abundance and observation error. Regular summary reports in ADFG's *Fishery Data Series* document the details of the annual estimates (e.g. Jones, Reed and Brandenburger 2012; Jones et al. 2006; Yanusz et al. 2000; Yanusz et al. 1999; McPherson et al. 1998). Below we give a brief overview.

2.1.1.1. Spawner Estimates

Annual abundance of adult Coho Salmon crossing the Canada-US border is estimated based on a mark-recapture (MR) program jointly implemented by ADFG, DFO, and the Taku River Tlingit First Nation.

Returning adult Coho Salmon are captured, measured, and spaghetti-tagged at Canyon Island (located in the lower Taku River just downstream from the Canada-US border), using two fishwheels with sample sizes augmented by using closely monitored set gillnet(s) when water levels are low late in the season. Scale samples are also collected and analyzed to estimate age composition. Canadian commercial and test fisheries, 3-20km upstream of Canyon Island, are then sampled for tags and scales. The Canadian commercial fishery is typically open from May/June until October, with Coho Salmon being harvested during directed Sockeye Salmon openings which occur June through early August and in Coho Salmon targeted fishery periods in August through September. The Canadian test fishery commences in September and is in place to increase tag recovery effort and is especially important as the sole recapture method after commercial fishers have vacated the river, generally after mid-late September. The test fishery is implemented with 2-3 boats under one scientific ("collection") licence and runs into early October.

The MR program typically runs from late April/early May (when it starts up to cover Chinook Salmon), through June to August when Sockeye Salmon are prevalent, to late September/ early October. The program covers all but the latter part of the Coho Salmon migration, which continues through the end of November; so late-timed returns are not fully sampled. Run timing models have been applied in some years to estimate the abundance of Coho Salmon not covered by the mark-recapture data (Pacific Salmon Commissions Joint Transboundary Technical Committee 2012).

MR estimates of Taku River Coho Salmon spawner abundance are available for 1987 to 2013 (Table A 1). Based on the sex ratio observed at Canyon Island, we calculated a time series of female spawners. For SR modeling, we rescaled this to effective total spawner equivalents based on a long-term median sex ratio of 40%.

2.1.1.2. Smolt Estimates

Annual abundance of Coho Salmon smolts is estimated based on a mark-recapture program conducted by ADFG and DFO.

Outmigrating Coho Salmon smolts are captured in traps over a 20km stretch centered close to Canyon Island. All live smolt are fin clipped and CWT-tagged (i.e. the marking event). Scale samples are also collected and analyzed to estimate age composition. The following year, the returning adults are sampled for marks (CWT) during port sampling, dockside creel surveys, and during the live-capture portion of the adult mark-recapture program at the Canyon Island fishwheels described above. These three sample sources constitute the recapture event which provides inputs for the smolt abundance calculation (Williams and Jones 2014, Jones et al. 2012).

Smolt estimates are available for 1990 to 2010 (Table A 1), but note that the sampling gear changed about midway through this period. Rotary screw traps were used exclusively through 1996, baited Gee minnow traps and screw traps in 1997, and minnow traps exclusively since 1998.

Annual smolt estimates are converted to brood year based on observed age composition in the juvenile scale sampling program. No alternative age composition data is available.

2.1.1.3. Catch, Run, and Recruitment Estimates

Alaskan harvests of Taku Coho originating above Canyon Island are expanded from CWT recoveries during port sampling and dockside creel surveys. Canadian in-river harvests are identified based on in-season catch monitoring. Catch estimates by sector are listed in Table A 3 for 1992 to 2013.

Annual adult returns are the sum of spawners and catches, and converted to recruits by brood year based on each year's observed age composition from scale samples collected during the mark-recapture survey.

The proportion of age 1.1 Coho Salmon tends to be substantially lower in the scale samples from the Canadian commercial and test fisheries (C&T) than in the samples from Canyon Island (CYI). The samples are processed in different labs, but both have well-established ageing protocols. ADFG scale samples for Taku Coho Salmon were recently re-analyzed by a single individual for all years of data, and double checked by 2 others. DFO samples were processed at PBS with very little staff turnover. Apart from potential biases in the age reading, a possible explanation for the observed difference is gear selectivity, with fishwheels tending to capture smaller fish than the drift and set-nets used in the commercial and test fisheries. Although the size differential between the age classes of Taku Coho Salmon is not very pronounced, the fishwheel sample is deemed to be more representative of the full distribution. However, this assumption has not been confirmed specifically for the Taku River Coho Salmon surveys. In addition, the time series for the CYI age composition database is more extensive than the C&T database (I. Boyce, DFO Whitehorse, pers. comm.). Due to these considerations, we use recruits based on CYI age composition for the base-case analysis, and alternate recruit estimates based on the C&T age composition as a sensitivity analysis.

2.1.1.4. Mark-Recapture Estimates and Observation Errors

Williams and Jones (2014) describe the survey and estimation methods for Taku River Coho Salmon. A brief summary follows below. Table A 2 lists the estimated observation errors for the base-case data set.

Abundance of adult Coho Salmon is estimated from the mark-recapture sample using one of two alternative methods. If diagnostic test confirm the assumptions required for unbiased estimation, Chapman's version of Petersen's abundance estimator for closed populations (Seber 1982) is used, and standard errors (SE) are estimated based on bootstrapping. If the estimate needs to be stratified based on area or time, then estimates of abundance and SE use the approach of Darroch (1961) as implemented in the software package SPAS by Arnason et al. (1996).

SE for annual recruitment estimates are based on a combination of estimated SE for the component variables: spawner abundance, harvest, and age composition. SE for harvest estimates in each fishery is derived from bootstrapping of the stratified coded-wire tag estimates (Bernard and Clark 1996), and variances are summed across fisheries to get a SE for the total harvest estimate (Jones et al. 2012). Brood year information that is assigned to marine harvest is based on the age composition estimates from the CYI samples. SE for age composition is based on the standard variance formula for proportions (Eq. 10 of Williams and Jones 2014). SE in total recruits is based on the sum of variances for each age class, which in turn is calculated based on SE age composition and run size, which is based on sum of variances for spawners and harvest.

2.1.2. Exploratory Data Analysis (EDA) for the Taku Coho Stock Aggregate

Figure 1 shows all the data used for the analyses presented in this report. Figure 2 shows the same time series, with observation error and rescaled time series that isolate the underlying signal using ranked deviations from the median (Section 12.1). Spawner abundance declined in the late 1990s, peaked in the early 2000s, and then dropped to the long-term median. Smolt abundance follows the same pattern, just offset a few years because the increasing smolt abundance results in increased spawner abundances when they return 1-2 years later. Adult recruit estimates also follow a similar overall pattern, offset from the spawner abundances just as the smolt data. Note, however, that the smolt abundance stayed consistently above average throughout the 2000s, while spawner and recruit estimates show a clear dip. This disconnect is unexplained at this time, but helps to interpret differences in SR model fit. Potential explanations that could be further explored include that the difference in pattern is simply a spurious artefact due to the larger observation error in some years (Table A 2) or that there are real underlying mechanisms resulting in complex interactions between spawner abundance, smolt abundance, smolt size, smolt age composition, adult age composition, and smolt-to-adult survival, which are potentially further complicated by differences among the subcomponents of the stock aggregate from different parts of the watershed. The middle part of Section 4.2 discusses this discrepancy between smolt data and adult data with a focus on the resulting differences in estimates of biological benchmarks.

Figure 3 shows raw productivity patterns based on the alternative data sets in Figure 2, with raw productivity defined simply as the ratio of offspring/parent without adjusting for abundance of parents. The 6 possible variations show roughly the same pattern over time, with distinct peaks in the late 1980s, late 1990s, and late 2000s. Figure 4 summarizes all the patterns and shows that the underlying productivity pattern is the same for all 6 variations shown in Figure 3, and that productivity has the opposite pattern of abundance, indicating strong density dependence.

Figure 5 shows pairwise scatterplots of the 6 alternative data sets which form the basis for Spawner-Recruit analysis.

Basically, the different SR models fitted in this paper are all attempts to explain the patterns in Figure 4 by fitting different lines through the scatterplots in Figure 5. The observations from 2002 and 2003, with the largest observed spawner abundances, are isolated from the rest of the scatter, and are therefore likely to have a strong influence on the model fits. The scatterplots in Figure 5 also capture the information content of the available data (as per Walters and Hilborn 1976, Clark et al. 2009). Points on the left side of the plots, above the replacement line contain information about the intrinsic productivity of the stock, while points on the right should ideally be scattered above and below the replacement line to capture information about the capacity.

Each of the data points in Figure 5 is a combination of two uncertain estimates. Figure 6 shows the bivariate error distributions for each observation. Some data points are clearly more uncertain than most of the others. For example, 2002 had the largest observed spawner abundance, and associated uncertainty is much larger than for the 2003 data point with the second largest spawner abundance (second from the right). Also note that data points can be more uncertain along one of the axes (e.g. 1999 has a vertical scatter indicating that the recruit estimate is more uncertain than the spawner estimate, 2008 shows the opposite pattern). Appendix Table A 2 lists the estimates and observation errors.

Figure 7 provides additional background for the biological analysis with a summary of overall harvest patterns from 1990 to 2013. Appendix Table A 1 lists estimates of total exploitation rate (ER) by year, and Table A 3 summarizes recent catches of Taku River Coho Salmon by fishery. Long-term median ER is 49%, with a distinct decrease throughout the 1990s and steady increase since the early 2000s. This ER pattern matches the total run in the early 1990s, with ER decreasing as abundance decreased. ER continued to decrease as abundance started to rebuild in the late 1990s, with lowest ER observed in the years of highest abundance since 1987 (2002, 2003). Since then ER has continued to increase as abundance dropped below the long-term median. Given that most of the ER is from Alaskan fisheries that are not specifically managed based on Taku River Coho Salmon abundance, this observed pattern is due to external factors affecting the dynamics of those fleets (e.g. weather, prices, water levels). However, this pattern also highlights the need for a bilaterally-agreed biological spawning goal.

2.2. APPROXIMATE GOALS FOR DATA-POOR SYSTEMS

2.2.1. Percentile Method for Identifying an SEG Range

This method identifies a biological reference range based on some percentiles of observed spawner abundance. ADFG has a step-wise algorithm based on contrast in the data (e.g. Table on p6 of Volk et al. 2009), while DFO has used 25th and 75th percentiles as the default (e.g. English et al. 2014). Both implementations refer back to Bue and Hasbrouck[1] and label the resulting range a Sustainable Escapement Goal (SEG).

This approach has been widely used for stocks that have a time series of spawner abundance but lack the information to estimate either juvenile production (e.g. smolt survey) or total adult returns (e.g. stock-specific catch estimates based on coded-wire tag recoveries)

Recent examples include:

- Volk et al. (2009) present 73 escapement goal recommendations for salmon stocks in the Arctic-Yukon-Kuskokwim region in Alaska: 59 of these (80%) are SEG based on the percentile method and 14 are BEG based on S_{MSY} estimates from a SR model fit.
- Most of the spawning goals reported as part of the ecocertification of BC Chum Salmon are SEG based on the percentile method (English et al. 2014).

Section 12.2 documents our implementation of the steps described by Volk et al. (2009) using the statistical package R (R Core Team 2013). First, round up spawner estimates to 2 significant figures, then choose the appropriate percentile range to calculate, based on the observed contrast in the data according to the following criteria, attributed to Bue and Hasbrouck[1]:

- if contrast <4 , then use 15% and largest observed;
- if contrast is ≥ 4 and <8, then use 15% and 85%; or
- if contrast is > 8, then use 75% for the upper bound and 15% for the lower bound if ER is low, or use 25% for the lower bound if ER is moderate to high. Volk et al. (2009) do not specify a cut-off between low and moderate ER, so our code in Section 12.2 calculates and reports both lower bounds.

Note that a recent simulation study (Clark et al. 2014) recommends using the percentile method only for stocks with low to moderate harvest levels (average ER < 40%). Clark et al. (2014) also propose a different set of break-points, but in our comparison we apply the approach above, which has been used for several large-scale ADFG reviews of spawning goals.

2.2.2. Smolt Capacity Method for Approximating S_{MSY}

This method identifies a biological reference range based on the average smolt abundance for large brood years, divided by regional average productivity. Shaul & Tydingco (2006) used this approach for two aggregates of surveyed Coho Salmon populations (Ketchikan, Sitka) with smolt abundance estimates based on marine survival and exploitation rate from a few indicator populations.

Section 12.3 documents the R implementation of the steps described by Shaul & Tydingco (2006), first extracting a subset of years with large spawner abundances, averaging the smolt estimates for those years, then dividing by a range of smolt/spawner values based on a regional review. We used their regional reference values of 25.4, 42.4, and 50.8 smolt /spawner for productivity at S_{MSY}, as well as the observed range for Taku River Coho Salmon of 14.6, 19.7, and 27.5 (25th, 50th, 75th percentile of observed smolt/spawner from 1990 to 2010).

2.3. BIOLOGICAL BENCHMARKS BASED ON SPAWNER-RECRUIT ANALYSIS

2.3.1. Spawner-Recruit (SR) Models

When estimates of adult recruitment are available in addition to spawner data, we can go beyond the approximate methods described in the previous section and use the observed interaction between spawner abundance and productivity to determine biological benchmarks.

The basic steps are to first choose a candidate model for the relationship between spawners and recruits, then estimate the model parameters from the observed data (i.e. fit a line through the scatterplots in Figure 5). By testing alternative model forms we can find out whether the conclusions are robust, or whether different starting assumptions produce widely differing results.

We fitted three alternative SR models (equations in Table 4):

- Standard Ricker model with density-dependence and log-normal errors (e.g. Bernard et al. 2000, McPherson et al. 2010, Grant et al. 2011, Holt and Ogden 2013);
- Extension to the standard Ricker Model to account for autocorrelation in residuals (i.e. series of good years and series of bad years) (e.g. Fleishman and Evenson 2010, Eggers and Bernard 2011, Fleishman et al. 2011, Hamazaki et al. 2012);
- Extension to standard Ricker model to account for changing productivity over time (i.e. varying alpha parameter) (e.g Peterman et al. 1998, Quinn and Deriso 1999, Peterman et al. 2000, Peterman et al. 2003).

Walters (2009) showed that the Ricker curve is a conservative default SR model for Coho Salmon, because *"when errors in variables and time series effects are large, assuming the Beverton-Holt model (f=ln(1+bS)) results in gross overestimates of productivity whether or not this model is the correct functional form. A conservative estimation tactic (to avoid risk of overestimating productivity and hence sustainable harvest rate) is thus to assume a Ricker model, and accept some downward bias in the productivity estimates for cases where the actual data were from a Beverton-Holt form of relationship."*

We fitted the three alternative Ricker models to six alternative data sets:

- *Spn2Ad*: Total spawners and adult recruits based on age composition from Canyon Island samples;
- *Spn2AdAlt*: Total spawners and adult recruits based on age composition from Canadian commercial and test fishery;
- *Spn2Juv:* Total spawners and smolts;
- *FemSpn2Ad, FemSpn2AdAlt, and FemSpn2Juv:* Same as the first three, except using female spawners rescaled to total effective spawners based on long-term average sex ratio of 40%.

Appendices B and C document the computer code used to calculate the SR model fits and associated benchmarks, which we implemented in the statistical package R (R Core Team 2013). The rest of this section briefly summarizes each step.

Figure A 2 shows QQnorm plots of log-transformed observations for each of the five time series (Figure 1) that are used in the six alternative data sets listed above. QQnorm plots compare the percentiles in an observed data set against the percentiles of a normal distribution, resulting in a linear pattern along the diagonal if the 2 distributions are similar. All are roughly log-normal, and we assume log-normal errors in all the SR model fits described below. Note, however, that both variations of the adult recruit estimates show some deviation from the lognormal distribution at the tail ends, and smolt estimates deviate even more.

2.3.2. Regression and Bootstrap (MLE+B) Method to fit SR models

Given current computing power and open source statistical packages like R, an initial check of the population dynamics can be quickly implemented using a linear regression estimate of the standard Ricker model parameters combined with bootstrap intervals to capture uncertainty. In some cases this may be sufficient, but in recent practice this is typically a first step before exploring other models (e.g. McPherson et al. 2010) or more complex estimation methods (e.g. Holt and Ogden 2013).

We estimated maximum-likelihood (MLE) parameters for the linear Ricker form, *ln(R/S)= ln(a) – bS*, with the simple linear regression function *lm()* in R (code in Section 12.4), then used the ln(R/S) residuals to create 5,000 bootstrapped data sets and re-estimated parameters for each.

To check for residual autocorrelation in each of the six alternative data sets, we applied the Durbin-Watson test using the *dwtest()* function of the linear model testing package *lmtest{}* in R.

Holt & Ogden (2013) point out that SR-based benchmarks may not be appropriate for populations with very low productivity, and recommend *Ricker a* < 1.5 as the criterion. We adopted their approach, and used the simple linear regression fits to verify whether subsequent Bayesian SR model fits are appropriate.

2.3.3. Bayesian MCMC Method to fit SR models

The main analyses for this report are based on Bayesian estimates using Markov Chain Monte Carlo (MCMC). This is the approach taken in most recent work on biological benchmarks for Pacific Salmon by ADFG and DFO (e.g. Brown et al.[2], Eggers and Bernard 2011, Grant et al. 2011, McPherson et al. 2010)

We implemented the MCMC using the BRugs package in R in combination with OpenBUGS (Thomas et al. 2006) but also cross-checked the results using the R2jags package in R in combination with JAGS (Su and Yajima 2014).

Our approach to MCMC estimation follows the methods described by Grant et al. (2010), and our BUGS code grew out of their long-evolving library of functions (Cass et al. 2006, Grant and MacDonald 2011, Grant and MacDonald 2012, MacDonald and Grant 2012).

Appendix B documents the BUGS/JAGS model code and Appendix C documents the associated R code, including key function calls from the BRugs() and R2jags() packages.

Table 6 summarizes the priors and settings used for each SR model variation. Table 7 summarizes the diagnostics we used to assess MCMC convergence and model fit.

2.3.4. Benchmark Estimation

For each bootstrap or MCMC sample of parameters, we calculated the estimated value of biological benchmarks S_{MSY}, S_{MAX}, and S_{EQ} based on the equations in Table 5, which are derived from the simplified calculation developed by Hilborn (1985). Benchmark definitions are listed in Table 1 and illustrated in Figure 8.

When calculating biological benchmarks, ADFG analyses typically apply a bias correction to the productivity parameter (e.g. Bernard et al. 2000, McPherson et al. 2010, Fleishman and Evenson 2010, Eggers and Bernard 2011, Fleishman et al. 2011, Hamazaki et al. 2012), but this has not been applied for the WSP benchmarks (Grant et al. 2011, Brown et al.2) and is not part of the WSP Software toolkit (Holt and Ogden 2013).

We used the bias correction as the base case in our analyses to stay consistent with other Transboundary analyses (i.e. McPherson et al. 2010 for Taku Chinook Salmon, Bernard et al. 2000 for Stikine Chinook Salmon, Eggers and Bernard 2011 for Alsek Sockeye Salmon), but present uncorrected estimates as part of the sensitivity analyses.

2.4. OVERVIEW OF SENSITIVITY ANALYSES

In addition to six alternative spawner-recruit data sets (Section 2.3.1) and three versions of the Ricker model (Sec 2.3.1), we also tested the sensitivity of SR model fitting approaches and resulting benchmark estimates.

The base case for all SR model fits was to use:

- all available years of data (1987 to 2009 brood years for adult recruits, 1990 to 2010 brood years for smolts);
- Bayesian MCMC estimates using BRugs() and OpenBUGS;
- Derived benchmarks based on the equations in Table 5 with bias correction on the productivity parameter.

Sensitivity analyses cover variations in the data set and variations in the estimation approach (Table 8).

We tested the effect of two resampling approaches:

- Retrospective: increase the time window used to fit the model starting with the 1987-1999 period and increasing it up to 1987-2009 for adult data sets, and starting with the 1990-1999 period and increasing it up to 1990-2010 for juvenile data sets.
- Jackknife: drop each observation and use the rest to fit the model

We compared the results from the following 4 alternative approaches to estimating derived biological benchmarks:

- Bayesian estimates using BRugs() and OpenBUGS;
- Bayesian estimates using R2jags() and JAGS;
- Regression-based estimates with bootstrap intervals (MLE+B);
- Using the software package developed by Holt & Ogden (2013) to estimate WSP benchmarks and metrics, which includes 80% S_{MSY}. Calculations are done in BUGS linked to the PBSModelling() Package in R. For now it includes only the standard Ricker model.

Finally, we checked derived S_{MSY} estimates against values calculated directly based on the largest median difference between recruits and spawners for 500 increments over the range [0,1.5* largest observed Spn].

2.5. PRESENTATION OF RESULTS

We present the results in various formats relevant to the two institutional frames of reference currently applied by ADFG and DFO (Section 1.3). This section describes the details of each summary.

2.5.1. Benchmark Ranges and Nonparametric Measures of Benchmark Precision

Key results from fitting SR models are probability distributions for each parameter, either based on bootstrap samples for the regression-based estimates (MLE+B, Section 2.3.2) or based on MCMC samples from the posterior distributions for the Bayesian estimates (Section 2.3.3). Using each of these sampled parameter sets in the benchmark equations listed in Table 5 gives corresponding distributions for S_{max}, S_{eq}, and S_{MSY}, which we summarize with the percentiles p10, p25, p50, p75, p90. In our notation, p# is the proportion of samples smaller than a particular value, such that, for example, p90= 89,000 means that 90% of the sample are smaller than 89,000 and 10% of the sample are larger than 89,000. Therefore p90 captures the upper tail of the benchmark distribution, with a high probability that this value meets or exceeds the true benchmark.

We also report three simple measures to summarize the spread in sample distributions:

- *Non-parametric Coefficient of Variation* (NPCV) = (p69.15-p38.85)/p50, which is the range that captures roughly the middle third of the samples divided by median. An estimate is considered precise if NPCV<25% (Clark et al. 2009);
- *Standardized Interquartile Range* (SIQR)= (p75-p25)/p50, which is the range that covers the middle half of the samples (i.e. the width of the box in standard boxplots), rescaled by median;
- *Standardized Median Absolute Deviation* (SMAD) = median of absolute residuals from median, divided by median.

Of these three variations, we use NPCV in subsequent comparisons (e.g. to rank by precision), because it is the only one with a published threshold (Clark et al. 2009). Note that NPCV and SIQR are only valid if the sample range does not span 0.

2.5.2. Yield Profiles

Recent ADFG reports with spawning goal recommendations (Section 1.3.5) include yield profiles that capture the notion of "pretty good yield" (PGY) as defined by Hilborn (2010).

We implement these plots as follows: at each increment of spawner abundance, we compare the distribution of yields (Rec-Spn) across parameter samples to the median yield at median S_{MSY}, and count the proportion that are larger. The resulting profile shows the probability of meeting or exceeding this average target, which is the number subsequent planning process will have in mind as an anchor point when choosing spawning goals. Note that our yield profiles differ from the version included in recent ADFG reports (e.g. Figure 10 in Eggers and Bernard 2011), which plot the probability of meeting the implied target for each parameter set (i.e. at each spawner increment, compare yield to MSY for that parameter set). The SR curves in Figure 9 illustrate the difference between these two approaches to calculating a yield profile. ADFG-type yield profiles are based on the bundle of Ricker curves in the top left panel, while our implementation uses the median SR curve in the bottom left panel as the comparison. Both approaches have the same intent and we consider them equally valid. They simply differ in the details of the calculation, and therefore we show both sets of results.

2.5.3. Recovery Profiles

Recent DFO reports with status assessments include estimates of S_{gen} as a key piece of information (definition in Table 1, description of status metrics in Section 1.3.5).

We show information relating to the lower benchmark for the *Relative Abundance* metric in a plot equivalent to the yield profiles described above. At each increment of spawner abundance, we compare the distribution of recruits across parameter samples to the median S_{MSY} and count the proportion that is larger. The resulting profile shows the probability of rebuilding to S_{MSY} in 1 generation in the absence of fishing, which is the basis for formal estimates of S_{gen}.

2.5.4. Summary Reference Points (SRP)

Yield and recovery profiles capture a lot of relevant information (e.g. shape of the curves), but are difficult to interpret across many sensitivity analyses.

We propose a suite of Summary Reference Points (SRP) that extract key information from these plots into a simple summary of biological reference ranges, capturing plausible interpretations of the benchmark distributions, yield profiles, and recovery profiles. For example, if S_{MSY} has 10th percentile at 64,000 and 90th percentile at 123,000 (Table 12, basic Ricker, Spn2Ad), these bookends reflect the same tail end of the distribution, but mean different things for subsequent planning. A spawner abundance (or goal) at 64,000 has a 90% probability of falling short of S_{MSY}, while 123,000 has a 90% probability of meeting or exceeding S_{MSY}.

The notation is Label#, with # indicating a percentile or probability level.

We propose the following SRP:

- SMSY50 = Median of MCMC posterior or bootstrap distribution of S_{MSY};
- LBM90 = the lowest spawner abundance that has a 90% or more probability of rebuilding to SMSY in one generation in the absence of fishing, Prob(Rec≥SMSY50), which is the point where the recovery profile crosses the 90% threshold, so that it reflects a 90% probability that this spawner abundance meets or exceeds the Lower WSP BM for *Relative Abundance*;
- UBM90 = 90th percentile of distribution for 80% SMSY50, which reflects a 90% probability that this spawner abundance meets or exceeds the Upper WSP BM for *Relative Abundance*;
- PGY90 = range of spawner abundances with 90% or more probability that the yield meets or exceeds 70% of MSY (median yield at SMSY50), which correspond to the segment of the yield profile above the 90% threshold.

As an illustration, we also report three arbitrary alternatives to PGY90, showing the range of spawner abundances with 60% probability of 70 % MSY, 80% MSY, or 90% MSY.

Note that these proposed SRP are not intended to be management reference points as defined by Holt and Irvine (2013); they are used only to compare a large number of sensitivity analyses side-by-side in a simplified summary that addresses both ADFG and DFO frames of reference.

3. RESULTS

Note: Our analyses focus on spawner-recruit models and biological benchmarks derived from the model fits, but include as a consistency check some methods used in data-poor systems. We present the results in a progression of increasing data requirements and analytical complexity.

3.1. APPROXIMATE GOALS FOR DATA-POOR SYSTEMS

3.1.1. Percentile Method for Identifying an SEG Range

Table 9 shows percentile-based SEG ranges calculated for all years of spawner data (1987-2013).

The approach used by ADFG in recent years produces a range of 56,000 to 130,000 Coho Salmon. This range is based on the 15th and 85th percentiles because contrast in the spawner observations is 6.7, which is a classified as a "medium" level of contrast according to the ADFG criteria (see Section 2.2.1, and Fair et al. 2011).

The DFO approach uses the 25th and 75th percentiles resulting in a SEG range of 62,000 to 120,000 Coho Salmon. This explains why the ADFG range is a bit wider.

Figure 10 illustrates how the estimated SEG ranges change when adding additional years (left panel) or dropping individual observations (right panel). The lower end of the range is highly robust to both sensitivity analyses, but the upper bound of the DFO SEG range increases substantially as data from the early 2000s is included.

The ADFG approach rounds up spawner observations to 2 significant figures first, but the DFO approach uses the raw data. Table 10 shows that SEG ranges are generally robust to alternative approaches to rounding, except for one special case where rounding affects the contrast and therefore noticeably reduces the upper end of the percentile range being calculated (see middle column of first row in Table 10 for data up to BY 1999).

3.1.2. Smolt Capacity Method for Approximating S_{MSY}

Table 9 shows S_{MSY} ranges for Taku Coho Salmon using regional reference values in Shaul & Tydingco (2006) based on including brood years with top 75th, 50th, and 25th percentiles of the observed spawner abundance. The resulting S_{MSY} ranges are similar, but point estimates of S_{MSY} increase from 48,000 to 54,000 Coho Salmon as the data set shrinks to include only large brood years.

The observed productivity of Taku Coho Salmon (bottom of Figure 3) is less than half of the regional reference values: the long-term median is 19.6 smolt/spawner compared to 42.4 used by Shaul and Tydingco (2006). Changing the productivity assumption to reflect actual estimates for Taku Coho Salmon more than doubles the mid-points of the approximate S_{MSY} ranges with the point estimates ranging from 104,000 to 117,000 spawners, compared to S_{MSY} point estimates that range from 48,000 to 54,000 spawners based on regional reference smolt/spawner values (Table 9).

3.2. BIOLOGICAL BENCHMARKS BASED ON SPAWNER-RECRUIT ANALYSIS

3.2.1. Sensitivity Analyses – 3 Models & 6 Data Sets

Table 11 lists results for regression-based point estimates of parameters for the basic Ricker model for each of the six alternative data sets and corresponding tests for serial autocorrelation. All 6 SR data sets have high intrinsic productivity ($a > 1.5$), so biological benchmarks can be calculated (Holt and Ogden 2013). All data sets also show very strong autocorrelation in residuals from the basic Ricker model.

The remaining results in this section are all based on Bayesian MCMC estimation using BRugs and OpenBUGS.

Figure 11 shows the SR fits for the base-case data set, with total spawners and adult recruits estimated from age composition in the Canyon Island data (Spn2Ad) for 3 variations of the Ricker model (see Section 2.3.1). Figure 12 to Figure 14 show how the SR curves link to biological benchmarks. Note that Figure 11 to Figure 14 use the Ricker Kalman SR curve for the most recent available brood year, which is 2009 for the Spn2Ad data set.

Table 12 lists percentile values for posteriors of S_{MSY}, S_{MAX}, and S_{EQ}, as well as simple indicators of precision for 3 Ricker model variations fitted to the base-case data set (Spn2Ad). Table 13 lists corresponding model fit, precision, and Summary Reference Points (SRP) for all 18 model-data combinations that we tested.

Figure 16 plots model fit (DIC) vs. precision (NPCV) for the 18 combinations of Ricker model variations and data sets. Figure 17 shows the shape of posterior parameter distributions for 3 variations of the Ricker model fitted to the Spn2Ad data set. Appendix D shows the same plot for the other 5 data sets. Figure 18 and Figure 19 show how the SR curve shifts by brood year for the Kalman-filtered Ricker model. Figure 20 compares the residuals for the 3 variations of the Ricker model, and Figure 21 shows the autocorrelation plots.

All three Ricker variations fit the Spn2Ad data well, and resulting posterior distributions are fairly precise (Figure 11, Table 12), with all NPCV < 25% (Clark et al. 2009).

The Ricker AR1 model corrects for autocorrelation in the residuals (i.e. series of good years or bad years). It is less influenced by the two observations from years with the largest spawner abundance, because they follow each other (2002, 2003), and therefore shifts to the left relative to the basic Ricker fit (Figure 11). The yield curve in Figure 12 shifts accordingly, and Ricker AR1 estimates a lower S_{MSY} than the standard Ricker model (69,000 vs. 79,000 spawners in Table 12).

The Kalman-filtered Ricker model fit for the Spn2Ad data set results in a time-varying SR curve, and the 2009 brood year shows below-average productivity (Figure 18, Figure 19). As a result, the Ricker Kalman SR curve in Figure 11 falls substantially below the other two Ricker variations, with corresponding lower yield curves (Figure 12), S_{MSY} (Table 12) and PGY profile (Figure 13). The recovery profile in Figure 14 shifts to the right, because lower productivity means that a higher spawner abundance is required to rebuild to S_{MSY} in 1 generation. However, it does not shift much relative to the basic Ricker model (34,000 vs. 32,000 spawners), because S_{MSY} has dropped (62,000 vs. 79,000 spawners).

The Deviance Information Criterion (DIC), summarized in Table 13, measures statistical fit based on the MCMC sample distributions as a combination of spread in the posteriors of all the model parameters and a penalty for additional parameters (Section 2.3.3). Models with better fit have lower DIC. For Taku River Coho Salmon, the Ricker Kalman model clearly has the best statistical fit (i.e. lowest DIC value) across all alternative data sets, but it introduces the additional complexity of time-varying benchmark estimates (Figure 19). The Ricker AR1 model greatly improves statistical fit for the juvenile data sets relative to the basic Ricker model, but the DIC comparison is inconclusive across alternative adult data sets (slightly better for Spn2Ad, the same for FemSpn2Ad, and slightly worse for the 2 AdAlt data sets). Both the Ricker and Ricker AR1 models fit the juvenile data sets poorly compared to adult data sets, and resulting S_{MSY} distributions are very wide (NPCV>25%). For the two variations of the juvenile data set, only the Ricker Kalman model results in S_{MSY} estimates that meet the 25% NPCV cut-off used by Clark et al. (2009).

The comparison of model fit and benchmark precision in Figure 16 highlights these differences. There are 3 clearly distinct clusters of results. In the first cluster, the 6 variations using juvenile data as the recruit variable are on the right side of the plot, with considerably worse fit (much higher DIC), and much lower precision in the resulting S_{MSY} estimate for the basic Ricker model (higher NPCV, above the 25% cut-off). Correcting for autocorrelation with the Ricker AR1 model greatly improves precision of these estimates (empty triangles lower than empty circles), but model fit actually worsens for the FemSpn2Juv data set. Ricker and Ricker AR1 models fitted to adult data are tightly clustered with similar model fits and benchmark precision. All fall below the 25% NPCV cut-off. The Ricker Kalman model fitted to adult data further improves model fit (third cluster, left side of Figure 16), but benchmark precision is similar to the other 2 Ricker variations.

The 3 Ricker model variations have a very pronounced effect on the distribution of log residuals, log(Obs Rec) – log(Fitted Rec for each MCMC sample), as shown in Figure 20. Including the autoregression correction (Ricker AR1), reduces the pattern in log residuals over time (left panel) and reduces the multi-modal peaks in the overall distribution (right panels). The Ricker Kalman model, which estimates brood-year specific productivity parameters, essentially removes all the residual pattern (Figure 20) and converts it into a productivity pattern (Figure 19).

3.2.2. Sensitivity Analyses - Alternative Calculation Approaches

We implemented the base-case analysis (Ricker, Spn2Ad) with several alternative calculation approaches to check robustness of the benchmark estimates. Table 14 summarizes the results.

3.2.2.5. BUGS vs. JAGS

The choice of alternative software packages for MCMC sampling has little effect on S_{MSY} estimates. Comparing row 1 to row 3 and row 2 to row 4 in Table 14 shows that results are very close, but not identical (i.e. within rounding to the nearest 1,000), except for the upper tail end of the posterior distribution (90th percentile), which affects the estimate of UBM90, the reference point with a 90% probability of meeting or exceeding 80% of S_{MSY}. For the basic Ricker model, a p90 of 123,000 spawners for the BUGS fit (Table 14) gives a UBM90 of 80% S_{MSY} at 98,000 spawners (Table 13), but the corresponding reference value for the JAGS fit is 95,000 spawners based on a p90 of 119,000 spawners (almost a 5% difference).

From a computing perspective, the two packages are almost identical. Small code tweaks were required to make r2jags() run for some models (e.g. the constraint on log.resid.0 ~ dnorm(0,tau.red) # I(-3,3) had to be removed for the Ricker AR1 model; Section 11.3). JAGS ran about 30% faster, making it the preferred option when crunching through many iterations in a sensitivity analysis (e.g. retrospective).

3.2.2.6. Bayesian MCMC vs. MLE+B

The choice of estimation method has little effect on median S_{MSY} estimates (row 1 vs. 5; row 2 vs. 6). The results for regression with bootstrap, which can be quickly implemented in a spreadsheet, are slightly lower than for the computing-intensive Bayesian fitting (e.g. 77,000 spawners vs. 79,000 spawners for the median S_{MSY}). However, the bootstrap intervals can be overly confident in the estimate. Among the 6 alternative data sets explored in this paper (Figure 5), this was especially pronounced for the Spn2Smolt. Table 15 compares SR fits for the Spn2Smolt data set with two alternative SR Models (Ricker and Ricker AR1) and over 2 time periods (1990-2001, 1990-2013). Bootstrap intervals for S_{MSY} are also much narrower than the Bayesian estimates during the early part of the retrospective evaluation for the Spn2AD data set (Figure 22).

3.2.2.7. Bias Correction

Bias correction on the Ricker α parameter (Table 5) increases the S_{MSY} estimates by a few percent (comparing "corr" with "raw" in Table 14, e.g. row 1 vs. 2). The magnitude of change is small for the median estimates which increase by approximately 5-8% for the four comparisons in Table 14. However, the bias correction also changes the shape of the posterior distribution by stretching out the upper tail (e.g. compare point estimates and bootstrap percentiles for corrected and raw MLE+B estimate in Table 14).

3.2.2.8. Holt and Ogden (2013) Toolkit

Holt and Ogden (2013) developed a software package (denoted H&O below) for estimating status metrics under Canada's WSP, which produces estimates of 80% S_{MSY} as the upper benchmark for the *Relative Abundance* metric and S_{gen} as the lower benchmark. Using the Spn2Ad data set for Taku River Coho Salmon, the H&O point estimate of S_{MSY} (70,000 spawners) using simple regression fits (MLE without bootstrap) is identical to our regression-based point estimate (comparing row 7 to row 6 in Table 14) without bias correction on the productivity parameter α (see Table 5 for bias correction). Comparing row 8 to rows 1 and 2 shows that the H&O median Bayesian estimate of S_{MSY}(72,000 spawners) is about 4% lower than our raw estimate (75,000 spawners using BRugs) and 8% lower than the corresponding bias-corrected estimate (79,000 spawners). Also note that H&O produces a much narrower posterior distribution (i.e. a lower p90). This difference is probably due to a combination of the way priors are set up in the two software packages and details of the implementation (e.g. at which step in the calculation parameters are rounded). Overall, H&O confirms our results for the subset of variations that match up (basic Ricker model, no bias correction).

Note that H&O estimates of S_{gen} range from 15,000 (p10) to 30,000 (p90) spawners, which closely matches our LBM90 estimate of 32,000 spawners for the same model and data set (Ricker, Spn2AD; Table 13). This is reassuring, given that we use a brute force calculation of LBM90 that is slightly different from the formal definition of S_{gen}, which H&O calculate by solving an equation (Holt and Ogden 2013). Note that our estimates of LBM90 and UBM90 include the bias correction Ricker α parameter which increases the S_{MSY} estimates by a few percent (previous section).

3.2.3. Sensitivity Analyses – Retrospective, Jackknife

Figure 22 shows the change in parameter estimates for the basic Ricker model as additional observations are added.

For the Bayesian MCMC fits (left panels), productivity ln(α) and capacity β are poorly estimated early on, with wide posteriors and shifting medians as new observations are included. The resulting S_{MSY} estimates are highly unstable and imprecise. The residual error σ and deviance steadily improve with each observation.

By comparison, the estimates based on simple regression and bootstrap are much more stable even with almost half of the data excluded (1987-1999 vs. 1987-2009). Bootstrap intervals are much narrower than MCMC posteriors for the early part of the retrospective before 2001, and the difference in perceived confidence (i.e. precision) is most pronounced for S_{MSY} estimates, which are the key output of these analyses and the anchor point for subsequent planning processes. Table 15 includes another example illustrating the magnitude of differences between bootstrap intervals and MCMC posteriors for the most extreme case, the Spn2Juv data set (1990-2010 data, basic Ricker model).

Figure 23 shows the change in parameter estimates for the basic Ricker model as individual observations are dropped from the data set, highlighting that no single data point has a drastic influence on the results. Residual error and deviance are visibly reduced by dropping either one of the low-productivity brood years (1993, 1994).

3.2.4. Sensitivity Analyses – Alternative Yield Profiles

Figure 15 compares two alternative approaches for developing yield profiles. The upper panels, labelled PGY, show the probability of achieving 70, 80, or 90% of median MSY at the overall median S_{MSY} (i.e. the yield profiles underlying the reference ranges in Table 13). The lower panels, labelled OY, show the probability of achieving 70, 80, or 90% of median MSY at median S_{MSY} estimate for each parameter set sampled from the posterior distribution (i.e. the yield profiles underlying the ADFG-type reference ranges). Table 16 compares the resulting reference ranges. Figure 9 illustrates the underlying reason for the difference: PGY yield profiles based on the overall median use the solid line in the bottom panel as the comparison; whereas the ADFG-type OY yield profiles use the bundle of curves in the top panel. Both approaches are intended to capture the uncertainty inherent in the posterior distribution.

Table 16 shows that this slight variation in the calculation of yield profiles has a drastic effect on the reference range that would be reported in a summary (e.g. for a bilateral process to choose a spawning goal). For example, with the same probability criteria, say 90% probability of 70% MSY, the first approach gives a reference range of 51,000 to 82,000 spawners (PGY for the Ricker AR1 model); whereas the alternative approach used in recent ADFG reports (OY 90-70 for the Ricker AR1 model) gives a much wider range of 35,000 to 98,000 spawners. For the wider range, the spawner abundance flagged as a potential concern is also much lower. Specifically, the lower end of the yield range is 35,000 spawners for the OY yield profile, but 51,000 spawners for the PGY yield profile (first row of Table 16). Note that the 90-70 values in Table 16 correspond to the vertical lines in Figure 15, and the specific example above refers to the changing width between the vertical lines in the right top panel and the right bottom panel.

4. DISCUSSION

4.1. DATA-POOR METHODS

Approximate goal calculations, such as the percentile method or smolt capacity method (Section 2.2), are used for data-poor populations which constitute the majority of Pacific salmon stocks (e.g. Volk et al. 2009, English et al. 2014). Stocks with additional information can be used to check whether these simple proxies are valid and provide background for the more complex analyses.

These simple proxies have some desirable properties, such as: they are clearly linked to the observed data; require no contentious assumptions about population dynamics; are very quick to apply; are easily communicated; and are insensitive to a few outliers in the data. For example, the 2002 and 2003 observations of high spawner abundances have a large pull on SR models as they try to estimate the capacity parameter (Figure 11), but the exact value of these observations is irrelevant in the percentile calculation. They only affect the overall contrast in the spawner data, which determines the range of percentiles to use (Table 10).

Note that exploitation rates affect the spawner pattern which is used as the sole information in the data poor approaches, and a pattern that is partly created by variations in ER is taken as biologically informative just by itself. For example, 2002 and 2003 were the years with largest observed spawner abundance, but 1991 and 1995 had the largest adult return (Figure 7). If ER had been substantially lower over the last 2 decades, the spawner percentiles would have been much higher. The version of the percentile method used by ADFG in recent years tries to account for this by adjusting the choice of percentile range based on contrast and ER level (Section 2.2.1). Benchmarks based on SR models try to account for this by assuming some underlying population dynamics (e.g. Ricker curve) and incorporating catches in the recruit estimates.

In practice, however, the two different sets of approaches can result in fairly similar reference ranges.

For Taku River Coho Salmon, averaging the two versions of the percentile method results in an SEG range of 59 to 125 thousand (average of first two rows in Table 9), centered close to the long-term average of 91 thousand (Appendix Table A 1). This is also roughly the same as the range from p10 to p90 for S_{MSY} derived from the basic Ricker fit for the Spn2Ad data set (Table 12), which covers 80% of the posterior distribution. Other model fits and other adult data sets result in similar or lower S_{MSY} estimates (Table 13); hence in our case study the percentile method produced a cautionary approximation of S_{MSY}.

As a contrast, the smolt capacity method, using regional reference values, results in an S_{MSY} estimate of approximately 50,000 spawners, which is substantially lower than most of the alternative estimates listed in Table 13. However, the observed productivity of Taku River Coho Salmon (bottom of Figure 3) is less than half of the regional reference values; the long-term median is 19.6 smolt/spawner compared to 42.4 used by Shaul and Tydingco (2006). In our case, changing the regional productivity assumption to reflect observed Taku Coho Salmon estimates more than doubles the mid-point of the approximate S_{MSY} range, highlighting that even simple approximate methods can be highly sensitive to underlying assumptions. However, if the subsequent decision process using the smolt-capacity results were to choose either the upper end of the range based on regional reference values (81,000 to 91,000 spawners) or the lower end of the range based on observed productivities (75,000to 84,000 spawners) as a management goal, then it would again closely match the SR-based S_{MSY} estimates.

Approximate methods for data-poor systems can produce cautionary and robust estimates (e.g. percentile method in this case), but can also widely miss the mark (e.g. smolt capacity method using regional averages in this case).

In a just-published paper, Clark et al. (2014) used simulations to test the properties of the 4-step percentile approach that has been used by ADFG for about decade (described in Section 2.2.1), and recommend a modified approach using a different set of criteria to choose percentile-based spawning goals. According to their evaluation, the use of the percentile approach is not recommended if the average harvest rate is larger than 40% (Taku ER = 48%, Appendix Table A 1). Further, if the average harvest rate *was* less than 40%, they recommend the appropriate percentiles now to be the 5th and 65th percentiles for a contrast of 8 or less, which they classify as low contrast (contrast in spawner abundance of Taku Coho Salmon = 6.7).

However, only a large sample of side-by-side comparisons of results for data-rich systems can truly verify the general properties of these approximate approaches and assist with the interpretation of results for the majority of systems where SR data is inadequate for model fitting.

4.2. BIOLOGICAL BENCHMARKS BASED ON SPAWNER-RECRUIT ANALYSIS

S_{MSY} estimates for Taku River Coho Salmon, which serve as the anchor point for both agency frames of reference, are remarkably consistent across alternative models for the adult base-case data set (Spn2Ad) and all available years of data (1987 -2009 brood years). Median estimates in these analyses range from 62,000 to 79,000 spawners differing by less than 30%

from each other (Table 12). Based on NPCV<25%, these estimates are considered to be fairly precise. For comparison, Grant et al. (2011) present estimates of 80% S_{MSY} ("Upper Benchmark") for many of the Fraser River Sockeye CUs that have substantially lower precision and larger differences between model types (their Table 4).

S_{MSY} estimates for Taku River Coho Salmon are highly robust to variations in the spawner-to-adult data (Table 13), but this observation is very specific to the particular data set currently available for Taku River Coho Salmon. For example, the two alternative assumptions about age composition (Canyon Island vs. Canadian commercial and test fishery) have little effect on SR model fit and resulting benchmarks (Spn2Ad vs. Spn2AdAlt in Table 13). Changing the age composition from Canyon Island to the commercial and test fishery data shifts the recruitment peak in the late 1990s back a year, and 3 of the observations change drastically (1998, 2006, 2007; see Figure 1); however, the overall scatter of spawner-recruit data points doesn't change much, and the two far-right observations from the 2002 and 2003 brood years don't change at all (Figure 5). This small difference between fits for adult data sets may not persist, and all the alternative data sets should be rechecked when our analysis is updated in a few years.

S_{MSY} estimates for Taku River Coho Salmon are highly stable across different estimation approaches including different software packages and whether or not to apply bias correction to the Ricker α. Seven alternative Ricker fits produce median S_{MSY} estimates that are within 11% of each other (Table 14).

The different biologically-based reference ranges listed in Table 13 can appear redundant at first glance, but they do produce very different results for some of the cases. For example, the spawner range with 90% probability of achieving 70% MSY (labeled PGY90 in Table 13) is essentially the same as the range with 60% probability of 90% MSY (last column of Table 13), for the Ricker and Ricker AR1 fits to the Spn2Ad data set (first and second row of Table 13); but, for the Ricker Kalman fit, one definition gives a range and the other definition doesn't (third row of Table 13. Figure 13 (lower left panel) illustrates that this is due to the shape of the yield curve, which doesn't rise above the 90% probability cut-off.

Note that the upper tail of these yield-based reference ranges is much more sensitive to alternative definitions and assumptions than the lower tail, just as observed when testing alternative model types and alternative data sets (Table 13). For example, UBM90 spans a range about 4 times as wide as the range in the upper bound of PGY90 (last row in Table 13). This observation that some reference ranges are much more sensitive than others needs to be considered when interpreting the results. Also note that the choice of method can have a very pronounced effect for some special cases. For example, S_{MSY} estimates based on juvenile data turned out to be highly sensitive to alternative estimation methods and choice of time period (Table 15).

SR model fits based on smolt data are much poorer than the adult fits (i.e. higher DIC in Table 13), but the effect on resulting benchmark estimates differs by model form. For example, the median S_{MSY} estimate (SMSY50) based on smolt data drops from 292,000 spawners for the basic Ricker model to 119,000 spawners for the Ricker AR1 version, and further to 96,000 spawners for the 2009 brood year of the Ricker Kalman fit. For the adult base-case data set (Spn2Ad), the same change in model structure only reduces the median S_{MSY} estimate from 79,000 to 69,000 spawners and then to 62,000 spawners. The patterns in Figure 2 show a clear disconnect between recruit estimates and smolt estimates during the mid 2000s, with above average smolt estimates and below average recruit estimates for the same brood year. This carries through to the results of the data-poor methods (previous section) and also affects the SR model fits. Several hypotheses could explain the observed discrepancies between juvenile and adult data. For example, if there was immigration of lower-river smolts (US origin), then smolt estimates would be biased high and actual abundance of Canadian-origin smolt would be lower. Alternatively, if the trapping methodology, which targets smolt rearing along the margins in the lower reaches of the Taku River, misses smolt that are outmigrating from more distant upstream locations, then the estimates would be biased low. Differences in migration characteristics between smolt from headwater streams and smolt produced from lower Taku spawning populations have not been examined. If the relative contribution of these opposing factors varies across years, a substantial disconnect could arise in some years. Finally, the discrepancies might be caused by fluctuations in smolt-to-adult survival, but formal modeling of this step is beyond the scope of the current analysis.

Lack of contrast is a common challenge when fitting spawner-recruit models (e.g. Collie et al. 1990). In the case of Taku River Coho Salmon, the spawning abundance in the 2002 and 2003 brood years greatly improve the contrast and strongly influence the spread of observations in the spawner-recruit scatterplots (Figure 5). However, had the ER been as high in 2002 and 2003 return years as it was in the 1991 and 1995 return years, this contrast would not have been revealed (Figure 7).

Our view of what constitutes a computing-intensive estimation method is changing rapidly as computers increase in speed and software packages make complex analyses more widely accessible. With today's tools, it is quick and simple to fit a linear regression and estimate bootstrap intervals based on resampling of residuals. The results from these analyses are valuable as a cross-check for the more complex, and therefore more error-prone, Bayesian estimates. Holt and Ogden (2013) have implemented this two-step approach in their software toolkit for estimating WSP status metrics. However, the simple bootstrap should not be used for determining biological reference points due to the potential for overly confident estimates (Table 14, Table 15, Figure 22). Note that more sophisticated bootstrapping approaches might address this concern (e.g. recreate serial autocorrelation in the residuals by resampling residuals only within distinct periods).

Recent implementations by the two agencies differ in their use of bias corrections on the productivity parameter (Table 5). Including the bias correction increases median S_{MSY} estimates and widens the posterior distribution (Table 14), which in turn affects some of the summary reference points used to interpret the biological information (Table 13). The question of when to apply this bias correction should be formally resolved (see suggested process in Section 5.4).

The three alternative measures of benchmark precision (NPCV, SIQR, SMAD; Section 2.5) all show the same pattern across alternative Ricker model forms (Table 12), and we use NPCV in subsequent comparisons.

Precision of the benchmark estimate (NPCV) roughly mirrors the statistical measure of model fit (DIC). The best fitting model (i.e. lowest DIC, ΔDIC=0) in Table 13 and Figure 16 is the Ricker Kalman model for the FemSpn2Ad data set, and it also produces the most precise S_{MSY} estimate (NPCV=10%). Overall, the worse fitting models also tend to have a wider spread in the resulting S_{MSY} estimate (i.e. the 4 model-data combinations with DIC > 10 all have NPCV >25%) The top panel of Figure 16 emphasizes this general pattern. However, the match in patterns breaks down between model fits with similar DIC, as additional parameters can introduce a disconnect between the two measures. For example, for the FemSpn2Juv data set, the Ricker AR1 has a poorer fit (higher DIC) than the basic Ricker model (i.e. the penalty for including an extra parameter exceeds the improvement in fit), but still produces a much more precise estimate of S_{MSY} (Table 13). Also note that the worst fitting model does not have the least precise estimate (i.e. in Table 13, the highest DIC is +52 for Ricker AR1 - FemSpn2Juv, highest ΔDIC is 157 for same model-data combination, but the highest NPCV is 145% for Ricker - Spn2Juv data. Comparisons are also confounded by the time-varying benchmarks of the Ricker

Kalman, where estimate precision changes by brood year: for different brood years in Figure 19, note the change in spread between the 25th and 75th percentiles of the posterior distribution.

4.3. CONSIDERATIONS FOR CHOOSING A SPAWNING GOAL

Policy shapes the frame of reference, which determines how we present and interpret the results of biological analyses. As summarized in Sections 1.3.3 and 1.3.4, ADFG and DFO operate under independent policies and the results of our analyses may be applied in different ways.

For example, the same biologically-based reference value of 98,000 Taku River Coho spawners (for Ricker fit to Spn2Ad data set; Table 13) could be treated as the:

- lower bound of the green status zone for the *Relative Abundance* metric under Canada's WSP (i.e. upper bound of the upper benchmark, which separates amber and green status zones). Any generational average larger than this is considered to be in the green status zone for this metric. Note however, that this does not necessarily result in an overall green status (Section 1.3.4);
- upper bound of the target range for the number of spawners that result in a pretty good level of sustainable yield (i.e. PGY90 = 55,000 to 98,000 spawners) under Alaska's SSP, with any long-term average larger than this indicating unfished harvestable surplus (Section 1.3.3).

Similarly, the range of 20,000 to 40,000 spawners (across all adult sensitivity analyses; bottom of Table 13) could be treated as the:

- range of LBM90, which is a threshold flagging concern. Spawner abundances below this value have less than 90% chance of recovery to S_{MSY} in 1 generation in the absence of fishing (~ S_{gen}). Note that the actual estimates in Table 13 range from 23,000 to 40,000 spawners).
- lower end of the range that is expected to produce a "pretty good" yield from the majority of brood years (i.e. 60% probability of 70% MSY), which could conceivably serve as the lower end of the escapement goal range for a stock where most of the harvest is taken in multi-stock fisheries, as is the case for Taku River Coho Salmon (Section 1.2.3). Note that the actual estimates of the lower end of the range with 60% probability of 70% MSY Table 13 vary between 29,000 and 37,000 spawners.

Reporting both of these frames of reference side-by-side highlights the fundamental differences in how policy could potentially affect outcomes. Similar comparisons for other salmon stocks will be required to determine the degree to which divergence in jurisdictional policies affects the interpretation and application of technical analyses. It may be that Taku River Coho Salmon are a special case where the differences are particularly pronounced.

Any analysis that only covers one or the other frame of reference would tend to push the policy discussion into a particular direction, which is clearly outside the mandate of this paper. Our analysis was prompted by the Transboundary Panel and the PST which obliged the Parties to "develop a joint technical report and submit it through the various Parties review mechanisms with the aim of identifying and establishing a bilaterally agreed to MSY goal for Taku coho". It will be up to the Panel to recommend how to bridge the policy-related differences in interpreting our results and arrive at a goal acceptable to the Parties.

Table 13 contains a number of options in response to the basic question: "What is a biologically-based spawning goal for Taku River Coho Salmon?"

The options originate from:

- 6 data sets (Figure 3, Figure 5);
- 3 models (Ricker, Ricker AR1, Ricker Kalman); and
- 5 different reference ranges (LBM90 to UBM90, PGY90, 3 more yield range variations).

This adds up to a total of 90 biologically-based reference ranges to choose from, plus sensitivity analyses, such as alternative calculation methods. However, once a planning process works through all the variations, the actual outcomes can be highly robust. For example, Grant and Pestal (2012) and Brown et al.[3] provided similar amounts of information to experts assessing salmon status in a workshop setting, where groups developed very different rationales for working through the information-intensive dashboard of status-related information, but often arrived at a consensus status designation after some facilitated debate.

Similarly, different rationales for setting a spawning goal may result in roughly similar ranges. If that happens, then the various planning processes can set aside the debate over theoretical differences and settle on an agreed-upon spawning goal.

For Taku River Coho Salmon, the Ricker Kalman model clearly has the best statistical fit (i.e. lowest DIC value) across all alternative data sets, but it introduces the additional complexity of time-varying benchmark estimates (Figure 19). If estimates of S_{MSY} vary from one brood year to the next, then any management goal based on S_{MSY} should shift accordingly. Even if the management system could find a process to work with goals that change every year, current productivity would still have to be forecasted from more than a generation earlier; but note that observed changes have occurred much faster. For example, Figure 19 shows that S_{MSY} estimates from the Ricker Kalman model can change from highest to lowest within 4 years.

The Ricker AR1 model greatly improves statistical fit for the juvenile data sets relative to the basic Ricker model, but the DIC comparison is inconclusive across alternative adult data sets (slightly better for Spn2Ad, the same for FemSpn2Ad, and slightly worse for the 2 AdAlt data sets), despite the strong autocorrelation found in the Durbin-Watson diagnostic (Table 11). Both the Ricker and Ricker AR1 models fit the juvenile data sets poorly compared to adult data sets, and resulting S_{MSY} distributions are very wide (NPCV>25%).

For the two variations of the juvenile data set, only the Ricker Kalman model results in S_{MSY} estimates which meet the 25% NPCV cut-off used by Clark et al. (2009).

Figure 24 compares two sets of benchmark estimates to observed spawner abundances. Recent median spawner abundance (71,000 spawners) is only slightly lower than the all-year median (74,000 spawners). Both medians are lower than the mean (91,000 spawners). Since the early 2000s, spawner abundance has mostly fallen into the range from roughly S_{MSY} to roughly S_{MAX}, with 2 observations reaching to roughly S_{EQ}. For the base-case data set, benchmark estimates for the basic Ricker fit are higher and more uncertain (i.e. wider posterior distribution) than for the Ricker AR1 fit which corrects for autocorrelation. However, the sensitivity analyses in Table 13 show that correcting for autocorrelation may either lower or increase the estimated biological benchmarks relative to the basic Ricker estimates, depending on which data set is used. For example, median S_{MSY} drops from 79,000 to 69,000 spawners for the Spn2Ad data set, but increases from 76,000 to 81,000 spawners for the Spn2AdAlt data set. The autocorrelation correction also affects the upper bound of yield-based ranges more than the lower bound. For example, the lower bound changes from 55,000 to 51,000 spawners while the upper bound changes from 98,000 to 82,000 spawners for the Spn2Ad data set (Table 13). This illustrates the need for extensive sensitivity analyses. If only the Spn2Ad data set had been tested, we might have come to erroneous generalizations about the relative properties of the alternative SR model forms.

Figure 25 compares the various reference ranges to observed spawner abundances. Recent and all-year medians put the spawner abundance of Taku River Coho Salmon squarely in the pretty good yield range, and near the boundary between the amber and green WSP status zones, *if our proposed Summary Reference Points were to be adopted (e.g. UBM90) and the results across adult SR model fits were selected for consideration from Table 13*. The long-term mean spawner abundance (91,000 spawners; Appendix Table A 1) falls more into the green status zone, but already exceeds some of the alternative values for the upper bound on the pretty good yield range. Finally, the decadal mean for 2001-2010 (129,000 spawners) is clearly above any of the adult-based UBM90 estimates, indicating that the relative abundance metric would have likely been assessed as green status under Canada's WSP for that period, but also falls substantially above the upper bound for the pretty good yield range, and therefore flags a substantial unfished harvestable surplus under Alaska's SSP.

Figure 26 compares observed spawner abundances to the alternative yield-based reference ranges, calculated using the same approach as recent ADFG reports. Figure 15 and Section 2.5 describe the differences between the two types of yield-based reference ranges. Figure 26 shows that spawner abundance has been in, or above, the ADFG-type optimum yield range in most years since 1987. The long-term median spawner abundance (solid line) falls near the upper end of the OY-90-90 range (i.e. 90% probability of 90% MSY) for the Ricker AR1 model recommended by CSAS, and just below the very narrow OY-90-90 range for the basic Ricker Model.

Considering only the various yield-based criteria, long-term average abundance over the last 26 years could be classified as close to the optimal. However, the time series shows that abundance was below optimal for most of the 1990s and above optimal for most of the 2000s *relative to current estimates of capacity based on a Ricker-type SR curve*.

Figure 27 compares observed ER to the estimated ER at maximum sustainable yield (U_{MSY}) and shows that ER has been below current estimates of U_{MSY} in most years since 1987. Note, however, that U_{MSY} is estimated ER at the S_{MSY} level of spawner abundance and should not be misinterpreted as fixed ER goal to use regardless of abundance. For example, the U_{MSY} estimate does not imply that Taku River Coho could be sustainably harvested at about 60% ER even if abundances drop to less than 10% of current spawner levels.

Figure 25 and Figure 26 also illustrate how much our perception of status can be influenced by seemingly minor details in the technical definitions (e.g. which measure of average or which probability level to use). There are two ways of addressing this issue: either present a large number of variations and find a way to pare them down to formulate final recommendations; or, reduce the number of variations at the onset by establishing a formal set of definitions and guidelines to be applied consistently.

The status summaries in Grant and Pestal (2012) are an example of the first approach, with benchmark information presented in 2 grids. Both grids compared current generational average abundance against biological benchmarks from up to 5 SR models at 5 different probability levels. One grid was based on the geometric mean and the other based on the arithmetic mean, for a total of 50 alternative metric values to consider (see dashboards in their Appendix 2). However, workshop participants were able to use the overall picture emerging from both grids to inform their status assessments.

The Summary Reference Points (SRP) we propose here (Section 2.5, Table 13, Figure 25, Figure 26) offer a step forward with the second approach. The bilateral guidelines we recommend in Section 5.4 could further simplify the results summaries for working papers that determine biological benchmarks for Pacific Salmon populations, especially if they fall under PST arrangements for transboundary management.

4.4. OTHER CONSIDERATIONS

From a broader perspective, the fact that spawner abundance exceeds one subset of S_{MSY} estimates for a period of time is not automatically a justification for increasing harvest levels. For Taku River Coho Salmon the following additional considerations might justify a buffer above the estimated values:

- Estimates in Table 13 are based on aggregate data for the entire Canadian-origin Taku Coho Salmon stock, and do not account for different intrinsic productivities of component populations that may at some future point be designated as distinct conservation units (Section 1.2.2);
- Estimates based on juvenile data are substantially higher than estimates using variations of the adult data. These could be considered in the goal-setting process even though they have poorer statistical fit;
- Posterior distributions for each biological benchmark span a wide range of values (Table 12). Using Ricker model results for the Spn2Ad dataset as an example, 80% of the posterior distribution for S_{MSY} ranges from 64,000 to 123,000 spawners;
- Sensitivity analyses identify variation in the inherent biological goal, both over time (Figure 22) and across model assumptions (e.g. SMSY50 in Table 13);
- Estimates in Table 13 are based on currently available information, but over the long-term there is a value of learning more about the population dynamics of Taku River Coho Salmon, especially with regards to spawning capacity. The effect of the 2002 and 2003 data points on alternative model fits highlight this in the current analysis (Figure 5, Figure 11). Clark et al. 2009 observed the same for Kenai Sockeye Salmon, and lack of contrast in spawner-recruit data is a common concern (e.g. Collie et al. 1990). A few more years of spawner abundances in the 200,000 range should improve the information content of the Taku River Coho Salmon data set.

Larger scale considerations for abundance-based management may also influence the choice of spawning goals. Specifically, the following considerations might support a wide goal range:

- *Implications for other fisheries:* The catch of Taku River Coho Salmon in SEAK Troll fisheries for Coho Salmon is the major driver of the exploitation rate on this stock. On average, the Alaskan troll catch comprises approximately 47% of the total harvest of Taku River Coho Salmon (Appendix Table A 3). However, given the small proportional contribution of Taku River Coho Salmon to the mixed-stock troll catch it is unclear how abundance-based management would be implemented in this fishery specifically to achieve a spawning goal for Taku River Coho Salmon. Given the current harvest pattern, the terminal gillnet fisheries would likely assume the greatest attention for addressing any short-term abundance concerns.
- *Management precision:* Given the complexities of mixed stock management and associated lack of management precision, a spawning target range of sufficient breadth that encompasses S_{MSY} and has buffer above S_{GEN} might be considered to be more risk adverse from a harvest-management perspective. Repeated failure to achieve the target range would require adjustments in ER. Under the current management regime, the ER has remained relatively conservative. However, a higher, but better defined spawning

escapement target combined with increased harvest pressure due to increased interest in fishing Coho Salmon, potentially could see this change.

- *Harvest variability:* In a system that is not directly and intensively harvested, a lower long-term goal may just reduce annual variability in harvest (i.e. fewer constraints on fisheries targeting other stocks or large aggregates).
- *Changing productivity:* Estimates of SR recruit parameters always lag behind changes in the environment, and a goal strongly influenced by the recent high abundance years may be overly optimistic about the long-term average capacity of the system.

4.5. SOURCES OF UNCERTAINTY

We evaluated the following sources of uncertainty:

- *Observation error:* Available data for the Taku River Coho Salmon aggregate are of high quality relative to other Coho stocks or CUs (i.e. have more than 20 years of consistent mark-recapture and CWT data). Figure 6 and Table A 2 summarize observation errors and show that estimates are generally quite precise, with some differences among data points. However, there may still be biases that affect the benchmark estimates, and future analyses could incorporate a more formal exploration of observation error by adding a Bayesian run reconstruction (e.g. Eggers and Bernard 2011, Fleischman and Evenson 2010).
- *Alternative data assumptions:* The analyses included 6 data variations capturing alternative assumptions about adult age composition, different life-history stages (adult vs. smolt), and effective spawner levels (total spawners vs. female spawners). Results were robust across adult data variations.
- *Alternative model forms:* The analyses included three variations of the Ricker model. All three assume that productivity declines at large spawner levels, but they differ in how they interpret observed productivity patterns. Results were robust across these model variations. Future assessment could explore other model forms for completeness (e.g. Beverton-Holt model which has no density-dependent decline at larger spawner levels).
- *Alternative estimation approaches*: Benchmark estimates were confirmed using different estimation approaches and software tools (e.g. comparison with output from WSP software package by Holt and Ogden 2014).
- *Policy interpretation and variations in technical details:* For a given set of results (e.g. a single model-data combination and estimation approach), the numerical estimates were sensitive to the alternative policy interpretations and technical details of summary calculations (e.g. yield profiles, summary reference points). Future analyses could be streamlined with clear guidelines for methodological details.

4.6. MANAGEMENT SYSTEM EVALUATION (MSE)

From a purely analytical perspective, the implications of all these considerations listed in Section 4.3 to 4.5 could be explored with an expanded model that implements a full Management System Evaluation (MSE), which is a simulation model with sub-models for:

- population dynamics (e.g. alternative Ricker models);
- harvest (e.g. dynamics of major fisheries harvesting Taku River Coho Salmon);
- assessment model (e.g. simulate alternative spawner survey coverage); and

- in-season management (e.g. abundance-based harvest rules).

The MSE could, for example, include alternative hypothetical population structures with 2 or 3 distinct conservation units of different productivity and run timing to explore the effect of a particular spawning goal and resulting harvest patterns (differential impacts on early vs. late timing components).

However, this work would constitute a major analytical effort, and its feasibility needs to be considered in the broader context of priorities for transboundary salmon management.

4.7. SUMMARY OF PROJECT OUTCOMES BY OBJECTIVE

Section 1.1 lists the 4 objectives for this project as identified in the original request for science advice. In this section we briefly summarize the outcomes for each objective.

Objective 1: Review the data & Objective 3: Examine and identify uncertainties in data and methods.

We consider these objectives covered off by the exploratory data analysis summarized in Section 2.1.2, which highlights the key features in the data to watch out for when interpreting the results, and the 6 data set variations we carried through the whole suite of SR analyses. Detailed discussions of the data are already documented in the ADFG reports cited in Section 2.1.1, and we considered it outside the scope of this project to revisit those analyses.

Figure 6 visualizes observation error in the SR data, and Table A 2 lists the corresponding values. Sections 4.5 and 5.1.1 discuss data quality, observation error, and resulting precision of biological benchmark estimates. Table 13 lists results for 18 sensitivity analyses (i.e. alternative model-data combinations).

Objective 2: Develop biological benchmarks at the aggregate level, including S_{MSY}.

The scope of our analysis was based on a broad interpretation of the Terms of Reference for the project. Therefore, we took the additional step of summarizing 3 alternative frames of reference (biological, ADFG, DFO; Section 1.3) and proposed a set of Summary Reference Points (SRP) to cover off all three. Our intent was to trigger a discussion, illustrate the implications of these alternative definitions, and hopefully lead to more specific guidance for future analyses (see Section 5.4).

Objective 4: Comment on future needs that would allow development of biological benchmarks at the CU level.

CU delineations for Taku River Coho Salmon are currently unresolved and we relied on the most recent published CU list which maintains a single CU (Section 1.2.2). Based on this, we de-emphasized this objective and included only some brief commentary in Section 5.2 rather than trying to develop a detailed discussion based on potential future CU delineations (e.g. sampling program required to develop CU-specific abundance benchmarks at some future time).

We also present estimates of WSP benchmarks at the aggregate level (e.g. Table 13) and discuss their implications (Section 5.3).

5. CONCLUSIONS

Note that this section summarizes 3 different sets of conclusions, which are clearly identified in each case: the authors (we); the CSAS-hosted peer-review process on Nov 3-4, 2014, in

Nanaimo (CSAS); and the Transboundary Technical Committee of the PSC during the Nov 19-20, 2014, meeting in Juneau (TTC).

5.1. BIOLOGICALLY-BASED SPAWNING GOAL FOR TAKU RIVER COHO SALMON

5.1.1. Quality of Information

Data available for the Taku River Coho Salmon aggregate are of high quality relative to other Coho Salmon stocks or CUs, with 23 brood years of consistent mark-recapture and CWT data (Section 2.1), as well as moderate contrast in spawner abundance (Section 3.1.1). CSAS and the TTC concluded that this data set is sufficient for fitting spawner-recruit models and using the resulting benchmarks as the basis for setting management goals.

A visual summary of observation errors shows that estimates are generally quite precise, with some differences among data points (Figure 6). Quantitative measures of precision confirm this assessment for both the input data (median coefficient of variation <10%;Table A 2) and the resulting biological benchmarks (non-parametric coefficient of variation <20%; Table 12).

Estimates of proposed summary reference points are remarkably consistent across many alternative models and data sets, with the most pronounced discrepancy found between adult and juvenile data sets (Table 13). However, there are substantial differences for some of the variations we explored, which confirm the need for extensive sensitivity analyses. The full suite of results needs to be considered in subsequent planning processes.

5.1.2. Recommended Model-Data Combination

Based on statistical and practical consideration, CSAS recommended one of the 18 model – data combinations as the most appropriate for developing management goals for Taku River Coho Salmon. Proceedings from the peer review (DFO 2015a) summarize the discussions and the Science Advisory Report (DFO 2015b) documents the resulting recommendations. CSAS also noted, however, that the rationale for using these SR model results in a status assessment might differ (e.g. one might choose to consider the range of estimates across several alternative model forms).

Specifically, the rationale was:

1. Set aside the juvenile results (six of the 18 model-data combinations), because they had consistently worse fits based on a standard statistical criterion and they also imply a different objective (i.e. maximizing smolt abundance is not the same as maximizing adult recruits);
2. Set aside the results for the Kalman-filtered Ricker model (four of remaining 12 model-data combinations), because they imply annual variation in S_{MSY} and their use would require a productivity forecast from the last available brood year. Kalman-filtered results may be useful for looking back in a status assessment, but given the complexities of international and mixed-stock management, it isn't practical to anchor management of Taku River Coho Salmon on a goal that changes annually;
3. Set aside results based on female spawners expanded to adult equivalents (4 of the remaining 8 model-data combinations). As with the Kalman-filtered results, these may be informative for status assessment, but are not practical for management purposes given potential challenges in refining in-season stock assessments and fishery monitoring programs to focus only on female Coho Salmon;

4. Set aside results for the alternative recruit time series based on age composition in the Canadian commercial and test fisheries (two of remaining four), because the age composition data from the Canyon Island survey is considered more reliable (longer time series available, mostly using fish wheel capture samples which is assumed to have lower size-selectivity).
5. Set aside the basic Ricker results (one of remaining two), because the strong observed autocorrelation in residual plots and the formal Durbin-Watson test points to the Ricker AR1 model as more appropriate.

Therefore, CSAS recommended the results for the Ricker AR1 model fitted to estimates of total spawners and adult recruits based on age composition from the Canyon Island survey as the main basis for management goals for Taku River Coho Salmon.

Estimated benchmarks and summary reference points for this recommended model-data combination are listed in the shaded middle column of Table 12 and shaded 2nd row of Table 13. A summary follows below.

Biological benchmarks (10th and 90th percentiles of the posterior distribution, capturing 80% of the parameter samples) based on data for the 1987-2009 brood years are:

- Spawner level that maximizes sustainable yield (S_{MSY}) estimated at 69,000 spawners (59,000 to 89,000 spawners);
- Spawner level that maximizes adult recruits (S_{MAX}) estimated at 107,000 spawners (82,000 to 154,000 fish);
- Equilibrium spawner level in the absence of fishing (S_{EQ}) estimated at 183,000 spawners (158,000 to 226,000 spawners).

Corresponding summary reference points are:

- Spawner level with 90% probability of meeting or exceeding 80% of S_{MSY} (UBM90, Upper WSP benchmark for *Relative Abundance* metric) estimated at 71,000 spawners.
- Spawner level with 90% probability of rebuilding to S_{MSY} in one generation in the absence of fishing (LBM90, 90th percentile of S_{GEN}) estimated at 23,000 spawners.
- Spawner range with 90% probability of achieving 70% of MSY at overall median S_{MSY} (PGY90) estimated at 51,000 to 82,000 spawners.
- Spawner range with 60% probability of achieving 90% of MSY at overall median S_{MSY} estimated at 51,000 to 84,000 spawners.
- Spawner range with 60% probability of achieving 70% of MSY at overall median S_{MSY} estimated at 30,000 to 110,000 spawners.
- Spawner range with 90% probability of achieving 70% of sample-specific median S_{MSY} (i.e. based on ADFG-type yield profile) estimated at 35,000 to 98,000 spawners.
- Spawner range with 90% probability of achieving 80% of sample-specific median S_{MSY} (i.e. based on ADFG-type yield profile) estimated at 43,000 to 89,000 spawners.
- Spawner range with 90% probability of achieving 90% of sample-specific median S_{MSY} (i.e. based on ADFG-type yield profile) estimated at 54,000 to 78,000 spawners.

Table 12, Table 13, and Table 16 show the corresponding estimates for other model-data combinations. A summary follows below.

Biological benchmarks for the Ricker AR1 model compare to the other estimates as follows:

- S_{MSY} and S_{EQ} are lower than for the basic Ricker model, but higher than for the 2009 brood year of the Kalman-filtered Ricker model;
- S_{MAX} is lower than for the basic Ricker model or the 2009 brood year of the Kalman-filtered Ricker model.

Corresponding summary reference points compare to the other model results as follows:

- LBM90 at 23,000 spawners is the lowest across 12 adult model-data combinations, which range up to 40,000 spawners;
- UBM90 at 71,000 spawners is among the lowest across 16 model-data combinations with estimates;
- PGY90 range at 51,000 to 82,000 spawners is the lowest across all 18 model-data combinations (i.e. minimum values for the lower and upper end of the PGY range in Table 13 are for the Ricker AR1 model fitted to the base-case data set Spn2AD);
- Across many, but not all, variations of yield-based ranges, the estimates for the Ricker AR1 model are lower than for the basic Ricker model (Table 16).

5.1.3. Recommended Spawning Goal

The TTC reviewed a draft of this document, endorsed the CSAS recommendation regarding the most appropriate model (see previous section), and came to a consensus technical recommendation for a biologically-based spawning goal of 70,000 total spawners, with a goal range from 50,000 to 90,000 total spawners.

Figure 28, Figure 29, and Table 13 establish the biological context for this recommended goal range. Figure 28 compares the goal to observed data. Figure 29 compares the goal range to model fits for the CSAS-recommended model-data combination (Ricker AR1 fitted to Spn2Ad). Table 13 lists the summary reference points estimated across sensitivity analyses (i.e. 18 model-data combinations, CSAS recommendation highlighted).

Comparing goal range to observed data:

- The left panel of Figure 28 shows that 3 early observations have fallen below the lower end of the goal range (1988, 1996, 1997), but most of the 27 available observations have been within (12 observation) or above (12 observations) the goal range.
- The right panel of Figure 28 shows goal range relative to the scatterplot of recruits vs. spawners, and highlights the wide range of observed recruit abundances for this comparatively narrow range of spawner abundances, with the range in recruitment about 6 times larger than the range in spawner abundance.
- Appendix Table A 1 shows that observed recruits varied from 91,319 to 289,431 fish for spawner abundances between 55,457 to 84,901 fish (i.e. the observed recruit values from escapements within the TTC recommended goal range). Also note that the two lowest observed recruitments were from brood years with spawner abundances slightly above the goal range (i.e. 1993 and 1994 data points below replacement line in right panel of Figure 28).

Focusing on the recommended model-data combination:

- A generational average (GenAvg) of spawner abundance of Taku River Coho Salmon in the upper half of the goal range (70,000 to 90,000 spawners) has a 90% or greater probability of being in the green zone for the *Relative Abundance* metric in a WSP status assessment (i.e. GenAvg larger than UBM90 in Table 13);

- A GenAvg in the lower half of the goal range (50,000 to 70,000 spawners) is in the amber or amber/green zone for the *Relative Abundance* metric (i.e. GenAvg below UBM90 in Table 13). Nearer to 50,000 spawners, it would be clearly amber. However, nearer to 70,000 spawners, it might be assessed as either amber, green, or amber/green status for this metric by different groups in a workshop setting, as was observed for similar information in the recent status assessment for Fraser River Sockeye Salmon (Grant and Pestal 2012);
- As long as GenAvg stays above the lower bound of 50,000 spawners the stock aggregate stays above the red status zone for *Relative Abundance* metric with a substantial buffer (i.e. GenAvg more than double LBM90 in Table 13);
- The goal range is centered on S_{MSY}, covers roughly the upper half of the spawner abundances up to S_{MAX}, and captures the peaks of all the yield-based profiles in Figure 29;
- The lower half of goal range (50,000 to 70,000 spawners) has a high probability of pretty good yield (70% MSY) and high yield (90% MSY). Towards the upper end of the goal range, yield drops considerably. There is still a high probability of pretty good yield but low probability of high yield. For example, the ADFG-type yield profile in the bottom right panel of Figure 29 shows that a spawner abundance of 90,000 is almost certain to get a yield of 70% of sample-specific MSY, but has only a roughly 50% chance of getting 90% of sample-specific MSY. Higher yield criteria result in narrower ranges (i.e. have to hit closer to the true S_{MSY}).

Considering estimates for all 12 adult model-data combinations (ranges at bottom of Table 13):

- The lower bound of the recommended goal range (50,000 spawners) is above all the alternative estimates for the lower benchmark of the *Relative Abundance* metric (LBM90); a GenAvg of 50,000 spawners or higher would not fall into the red status zone on this metric for any of the alternative estimates;
- The upper benchmark for the *Relative Abundance* metric (UBM90) is more sensitive to alternative model forms and data assumptions, with a range across sensitivity analyses that is wider than the recommended spawning goal range (i.e. UBM90 estimates range from 57,000 to 106,000 spawners);
- Yield-based reference ranges are sensitive to slight changes in definition (Section 3.2.4). The recommended spawning goal range closely aligns with the PGY90 ranges across sensitivity analyses, with estimates of the lower bound varying between 51,000 and 71,000 spawners and estimates of the upper bound ranging from 82,000 to 101,000 spawners (Table 13).

Note that the recommended spawning goal is substantially higher than the goal range of 27,500 to 35,000 Taku River Coho Salmon previously accepted by the Transboundary Technical Committee and Panel, which was based primarily on professional judgement and was in place up to 2013. The interim spawning goal of 70,000 fish, which was adopted by the Transboundary Panel in 2013 and implemented for 2014, is closer to our estimates of S_{MSY}. One reason for the discrepancy is the pronounced increase in both spawner abundance and adult recruits observed in the early 2000s (Figure 2). Harvest estimates based on CWT data have also greatly improved the ability to reconstruct annual runs and determine brood-year specific recruitment. Once analyses are updated to include this more recent information, the biological benchmarks go up (e.g. see retrospective pattern of S_{MSY} estimates in Figure 22).

5.2. FUTURE DATA REQUIREMENTS

Future data requirements are linked to population structure and management approach. For Taku River Coho Salmon this means that CU delineations and their implications for management need to be resolved.

In aggregate, Taku River Coho Salmon are not a data-poor stock. The analyses presented here were only possible because of the long-running mark-recapture programs for adults combined with the large-scale smolt tagging program to get marine catch estimates and smolt abundances. All of these programs need to continue to allow future updates of the benchmark estimates, and to potentially resolve some of the discrepancies across alternative assumptions. For example, the difference in age composition estimates from Canyon Island compared to data from the Canadian commercial and test fisheries currently has very little effect on the resulting benchmark estimates, because the 2 influential observations from 2002 and 2003 are not affected (Figure 5). However, this could change with any new observation, and both data streams should be maintained until the discrepancies are fully explained. Sampling gear selectivity studies would help to improve the integrity of whichever data source is selected.

If 2 or more distinct conservation units are confirmed for Taku River Coho Salmon, additional data collection at a finer spatial resolution needs to be considered within the broader context of coastwide assessment priorities.

The CSAS peer-review or Transboundary Technical Committee did not make any formal recommendations regarding this, but we suggest the following 4-step approach:

1. Compile and review all available information, including local knowledge and anecdotal observations (e.g. spawning distributions, timing, life history differences) to determine whether it is likely that Taku River Coho Salmon include more than 1 CU under the WSP.
2. If it is considered likely that there is more than 1 CU, explore the feasibility of assessments at a finer spatial scale within the context of coastwide salmon assessment priorities.
3. Formally confirm the CU delineations for Taku River Coho Salmon and complete WSP status assessments (next Section).
4. Then develop a bilateral stock assessment plan that accounts for CUs.

5.3. STATUS OF TAKU RIVER COHO SALMON

A formal status assessment under either policy is outside the scope of this paper, and neither the CSAS peer review nor the Transboundary Technical Committee developed status commentaries. In this section we offer a brief summary of likely outcomes to assist with prioritizing future assessments.

The two institutional frames of reference (Section 1.3) might look at same biological information and still come to different conclusions. Under Canada's WSP, there is no status metric related to yield and any spawning abundance above the upper benchmark for *Relative Abundance* would be in the green status zone for that metric. Under Alaska's SSP, status assessments include considerations of potential yields, with the implied notion of over-spawning, and resulting concerns over foregone economic opportunities.

An assessment under Alaska's SSP would probably come to the conclusion that spawner abundance for most of the last 15 years exceeded a Biological Escapement Goal (BEG) set at any of the reference ranges in Table 13, which indicates a very conservative management system and persistently foregone harvest opportunities (Figure 26). Note, however, that this would not constitute a yield concern, because in most years there was a harvestable surplus as defined by the policy (i.e. spawners in excess of S_{MSY}).

Assessments of biological status under Canada's WSP are done at the level of conservation units (Section 1.3.4) and focus on 3 standardized status metrics, which are relative abundance, extent of decline, and short-term trend, as well as a supplementary estimate of probability of decline.

Taku River Coho Salmon are currently delineated as a single CU, and at this aggregate level, available data are sufficient to calculate and assess all 4 of these metrics. However, some of the supplementary information used in recent WSP status assessments is not available for Taku River Coho Salmon at this time (e.g. changing relative contributions of sub-populations).

For the recommended data-model combination, the Upper and Lower Benchmarks (BM) for the *Relative Abundance* metric are 71,000 spawners (UBM90; 90% probability of meeting or exceeding 80% of S_{MSY}) and 23,000 spawners (LBM90; 90% probability of rebuilding to S_{MSY} in one generation in the absence of fishing, 90th percentile of S_{GEN}). Table 13 lists the corresponding values for the other model-data combinations, with UBM90 ranging from 57,000 to 106,000 spawners and LBM90 ranging from 23,000 to 40,000 spawners across 12 model-data combinations (i.e. excluding estimates based on juvenile data sets).

Two of the 3 status metrics would likely show green, because spawner abundance has been at, or above, S_{MSY} for more than a decade (Figure 24 and Figure 25) and recent median abundance is roughly the same as the long-term median (Table A 1, Figure 24). The decline from peak spawner abundance in 2002 might trigger amber or red status on the *Short-term Trend* metric, but expert evaluations in a workshop setting would weigh this against the other metrics and consider the associated patterns in exploitation rate and productivity before arriving at a status designation. Based on recent status assessments for CUs with similar data quality and observed patterns (Grant and Pestal 2012), we anticipate that biological status would likely be assessed as good during most of the 2000s, with a potential concern arising out of recent declines coupled with increasing ER (Figure 27).

We consider the first priority for WSP implementation for Taku River Coho Salmon to be the resolution of population structure. Once the CU delineations are finalized, a formal status assessment can be undertaken. If a single CU is confirmed, the data and SR models presented in this paper cover most of the required information. If, however, future investigations indicate more than one CU exists for the Taku River Coho Salmon aggregate, SR-based assessment of WSP status may not be possible and other status assessment approaches would have to be explored.

We also recommend that the broader challenge of reconciling the 2 policy frameworks in the management of transboundary stocks is formally tackled at the same time, rather than waiting until separate status assessments are completed under Canada's WSP and Alaska's SSP.

As an illustration of the issues, consider the following question: How would the bilateral management process respond if Taku River Coho Salmon were split into 3 distinct CUs, which are then assessed as *Data Deficient* because data are not available to estimate abundance or biological benchmarks at that resolution?

5.4. GUIDANCE FOR FUTURE WORK

During the scoping phase of this project we encountered enough variation in methods between ADFG and DFO (Section 1.3.5) to warrant considerations for a bilateral process that resolves them.

For example, the large variety of options we present in Table 13 results from our attempt to anticipate the likely suite of variations that participants in multiple subsequent planning processes might want to have available for their deliberations (agencies, Technical Committee, Panel), based on recent working papers from the two agencies. However, if clear bilateral guidelines were available, the results presented in future Transboundary analyses could be streamlined to these agreed-upon pieces of information.

Even the simplest method has variations that lead to divergence in agency practice without a common set of guidelines, as shown in the current differences in the percentile method for determining SEG ranges (Section 2.2.1). Many conceivable variations are possible (e.g. SEG for different regimes in longer time series).

Similarly, we consider the two variations of yield profiles (Figure 15) to be equally valid, but they produce different reference ranges (Table 16). The difference is not in intent or concept, but purely a matter of calculation details. We don't think that there is a formal criterion for choosing one over the other, but one version should be formally adopted.

If there were bilateral agreement on the technical details (e.g. bias correction, MCMC implementation), then the number of sensitivity analyses could be greatly reduced and the summary of results could be more tailored to the specific requirements of the transboundary planning process.

Note that CSAS and the TTC considered the various alternative summaries informative, but neither process formally endorsed our proposed summary reference points or recommended a particular subset of metrics.

A document summarizing guidelines for the development of biological benchmarks and management reference points for Canada/US Transboundary stocks could be based on recent practice by both agencies and include the following components:

- Reconcile the 2 agency frames of reference into a single transboundary policy statement (i.e. a "rosetta stone" for policy jargon, building on our brief comparison in Section 1.3);
- Build a decision tree for choosing among approaches for developing reference ranges (e.g. under which circumstances to use the percentile method, smolt-capacity method, or SR-based benchmarks);
- Compile best practices for estimating SR-based benchmarks (e.g. when to use bias correction on productivity parameter, determine a standard suite of alternative models to test, identify the minimum scope of sensitivity analyses, map out an updating process for reviewing and incorporating new approaches);
- Compile a manual for implementing and reporting Bayesian parameter estimates based on Markov Chain Monte Carlo. For example, Korman and Tompkins (2014) present extensive diagnostics based on residuals (e.g. χ^2 test for goodness-of-fit) that are not included in any of the ADFG or DFO reports listed in Section 2.3.3. A common checklist and implementation handbook would increase the consistency of future analyses.
- Agree on a standard set of reference ranges and summary plots to be presented (e.g. the summary reference points we propose in Section 2.5 and use in Table 13).

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8. TABLES

Table 1: Definition of Biological Benchmarks

Label	**Definition**
S_{MAX}	Spawner abundance that maximizes recruits
S_{MSY}	Spawner abundance that maximizes sustainable yield (Rec-Spn)
S_{EQ}	Long-term equilibrium spawner abundance in the absence of harvest
U_{MSY}	Harvest mortality rate at MSY
S_{GEN}	Spawner abundance with a high probability of rebuilding to S_{MSY} in 1 generation in the absence of harvest

Table 2: Matching 3 Frames of Reference for Spawner Abundance of Pacific Salmon. Evaluations are based on a chronic inability to meet the target (ADFG) or average generation time (DFO). In practice, both definitions result in a 4-5 year time window for most salmon stocks. Note that DFO Status Zones for relative abundance only reflect one of a suite of status metrics that need to be evaluated together. Sources and definitions listed in Section 1.3.

Biological Range	**ADFG Level of Concern**	**DFO Status Zones**
$> S_{MSY}$	Unfished harvestable surplus*	Green: No concern indicated by *Relative Abundance metric*, but integrated status not automatically green. (> 80% S_{msy})
$\approx S_{MSY}$	Goal	
$< S_{MSY}$	Management concern	Amber
Multiple criteria and formalized process	Conservation concern (below level where "sustainability is jeopardized")	Red (Relative abundance metric falls below S_{gen})

* Note that a yield concern under the Alaska's SSP only arises if spawning goals are being met, but there is no harvestable surplus available (e.g. when managing to a long-term average S_{MSY} goal during a period of reduced productivity). Unfished harvestable surplus is not considered a sustainability concern under the policy.

Table 3: Comparison of recent ADFG and DFO salmon policy implementation. References for recent implementation examples are listed in Section 1.3.

Aspect	ADFG	DFO
Focus of recent work	Spawning goals	Biological status (status benchmarks explicitly defined as NOT goals)
Population level	Stocks delineated based on management and assessment	Conservation Units delineated based on biological characteristics (genetics, life history, migration timing, freshwater and marine adaptive zones)
Assessment Process	Peer-reviewed status assessments (ADFG Fishery Manuscript Series)	Peer-review of available data and status metrics, followed by expert workshop to develop integrated status designations (CSAS Research Documents)
Harvest Planning Process	Status assessments reviewed by Alaska Board of Fisheries	IFMP, IHPC consider status, plan accordingly
Progress Highlights	Several state-wide reviews of escapement goals (2004, 2007)	Comprehensive status assessments of 3 high-priority CU groups (Fraser Sockeye, Southern BC Chinook, Interior Fraser Coho)

Table 4: Alternative Spawner-Recruit (SR) Models

Model	**SR Function**	**Description**
Ricker	$\ln(R) = [\ln(\alpha) - \beta S] + \ln(S)$	Standard Ricker model with density-dependence and log-normal errors (e.g. Bernard et al. 2000, McPherson et al. 2010, Grant et al. 2011, Holt and Ogden 2013)
RickerAR1	$\ln(R) = [\ln(\alpha) - \beta S + \phi\varepsilon_{y-1}] + \ln(S)$	Extension to the standard Ricker Model to account for autocorrelation in residuals (i.e. series of good years and series of bad years) (e.g. Fleishman and Evenson 2010, Eggers and Bernard 2011, Fleishman et al 2011, Hamazaki et al. 2012)
Ricker with Kalman Filter	$\ln(R_y) = [\ln(\alpha_y) - \beta S_y] + \ln(S_y)$ $\ln(\alpha_y) = \ln(\alpha_{y-1}) + \omega_y$	Extension to standard Ricker model to account for changing productivity over time (i.e. varying alpha parameter) (e.g. Peterman et al. 1998, Quinn and Deriso 1999, Peterman et al. 2000, Peterman et al. 2003)

Note: the Function column shows the model form used in the Bayesian estimation code (Appendix B).

Table 5: Derived Estimates of Biological Benchmarks. Biological benchmarks are calculated for each parameter set (MCMC or bootstrap) based on the derived equations below. In addition, Table 14 compares these derived BM estimates to calculated benchmark estimates based on a brute-force computation (Section 2.3.4). Note: for Ricker AR1 and Ricker Kalman the bias correction occasionally results in a negative Smsy (typically less than 10 out of a 1000 MCMC samples). These are discarded from subsequent analyses.

Model	**Smax**	**Seq**	**Smsy**	**Umsy**	**Bias Correction**	**Source**
Ricker and Ricker with Kalman Filter*	$\frac{1}{\beta}$	$\frac{\ln(\alpha)}{\beta}$	$S_{eq}(\ 0.5 - 0.07\ln(\alpha)\ )$	$\frac{S_{msy}}{\beta}$	$\ln(\alpha') = \ln(\alpha) + \frac{\sigma^2}{2}$	With Bias Correction: McPherson et al. (2010), Bernard et al. 2000 / Without bias correction: Grant et al. 2011, Holt and Ogden 2013
RickerAR1	$\frac{1}{\beta}$	$\frac{\ln(\alpha)}{\beta}$	$S_{eq}(\ 0.5 - 0.07\ln(\alpha)\ )$	$\frac{S_{msy}}{\beta}$	$\ln(\alpha') = \ln(\alpha) + \frac{\sigma^2}{2(1-\phi^2)}$	Fleischman and Evenson (2010)

* For Kalman Filter, use one of the brood-year-specific α_y. The results shown in the rest of this report are based on the last available brood year (2009 for adult recruits, 2010 for smolts), unless explicitly stated otherwise.

Table 6: Priors and MCMC Settings for Bayesian Estimates. Priors are implemented in the BUGS/JAGS code in Appendix B. Settings are used in the BRugs and R2jags function calls as illustrated in Appendix C.

Model	Priors	Settings	Sources
Ricker	$\alpha \sim$ lognormal(0,0.0001) $\beta \sim$ 1/lognormal(0,0.1) $\sigma \sim$ 1/sqrt(τ) $\tau \sim$ gamma(0.001,0.001)	2 chains with 80,000 burn-in and 40,000 retained MCMC samples each. Thinning =2 for diagnostics and 40 for extracted MCMC samples used in subsequent calculations (i.e. n= 2,000)	Adapted from code used by Grant et al. (2010)
RickerAR1	$\alpha \sim$ lognormal(0,0.0001) $\beta \sim$ 1/lognormal(0,0.1) $\sigma \sim$ 1/sqrt(τ) $\tau \sim$ gamma(0.001,0.001) $\phi \sim$ normal(0,0.0001) I(-1,1)	2 chains with 100,000 burn-in and 40,000 retained MCMC samples each. Thinning = 2 for diagnostics and 40 for extracted MCMC samples used in subsequent calculations (i.e. n= 2,000)	Adapted from a combination of two BUGS implementations: Code used by Grant et al. (2010) and Appendix A2 of Fleishman and Evenson (2010)
Ricker with Kalman Filter	$\alpha_y \sim$ lognormal(0,0.0001) $\beta \sim$ lognormal(0,0.1) $\sigma \sim$ 1/sqrt(τ) $\tau \sim$ gamma(0.001,0.001)	2 chains with 80,000 burn-in and 40,000 retained MCMC samples each. Thinning = 2 for diagnostics and 40 for extracted MCMC samples used in subsequent calculations (i.e. n= 2,000)	Adapted from code provided by Catherine Michielsens.

Table 7: Checklist of MCMC diagnostics. The following standard diagnostics were used to assess MCMC sampling and model fit.

Consideration	Diagnostic	Thresholds	Examples
Parameter estimates	Shape of posteriors	Check whether posterior distributions are smooth and whether they bump up against the limits imposed by the priors (i.e. appear cut off)	-
Convergence	Trace plot (sequence of sampled values) for each variable	Visual assessment of overlaid pattern for the 2 chains (check for adequate mixing)	-
Convergence	Change in Brooks-Gelman-Rubin statistic BGR (Brooks and Gelman 1998) with additional MCMC samples	Check whether initial conditions for the 2 chains are different from each other (large BGR) and then converge before the end of the burn-in, such that BGR over the length of the retained sample is between 0.9 and 1.1. Visually check plots and check numeric values over 50 bins on the thinned samples.	Grant et al. (2011)
Convergence	Geweke statistic G (Geweke 1992)	Check whether G falls within the range [-2, 2]. If not, then the earlier part of the MCMC chain differs from the later part and the samples didn't converge (G is a z score and values in this range indicate that early and late sample means fall within 2 standard deviations).	Grant et al. (2011)
Relative model fit	Deviance Information Criterion DIC (Spiegelhalter et al. 2002, Gelman et al. 2004)	Check relative difference in DIC to compare alternative model fits. Lowest DIC indicates best fit among the models considered, but does not show whether any of the models fit well or poorl	Grant et al. (2011), Korman & Tompkins (2014)

Table 8: Overview of SR Model Fitting Sensitivity Analyses. Base case for all SR model fits is to use all available years of data (1987 to 2009 brood years for adult recruits, 1990 to 2010 brood years for smolts). Sensitivity analyses cover variations in the data set and variations in the estimation approach. Abbreviations are as follows: MLE+B= Linear regression with bootstrap, BUGS = MCMC using BRugs and OpenBUGS, JAGS = MCMC using r2jags and JAGS, H&O = Holt and Ogden (2013) software package.

	RESAMPLING		**ESTIMATION**			
Model	**Incr. Time Window** (Retrospective)	**Drop 1 Observation** (Jackknife)	**MLE+B**	**BUGS**	**JAGS**	**H&O**
Ricker	X	X	X	X	X	X
RickerAR1	X	NA*	--	X	X	--
Ricker with Kalman Filter	X	NA*	--	X	X	--

* Ricker AR1 and Ricker with Kalman Filter require complete time series, preventing a direct jackknife evaluation.

Table 9: SEG Ranges for Taku Coho based on Methods for Data-Poor Systems. Sustainable Escapement Goals (SEG) are based on approximate methods for data-poor systems described in Section 2.2.

Label	SEG Range			Comment
	Lower Bound	S_{MSY}	Upper Bound	
Percentile Method				
ADFG	56,000		130,000	Use 15%-85% range, because contrast = 6.7
DFO	62,000		120,000	Use 25%-75% range
Smolt Capacity Method – Regional Reference Values of Shaul and Tydingco (2006)				
Top 75%	40,000	48,000	81,000	Drop smallest quarter of brood years
Top 50%	41,000	49,000	81,000	Use larger half of brood years
Top 25%	45,000	54,000	91,000	Use only largest quarter of brood years
Smolt Capacity Method – Taku River Coho Observed Values				
Top 75%	75,000	104,000	140,000	Drop smallest quarter of brood years
Top 50%	75,000	105,000	141,000	Use larger half of brood years
Top 25%	84,000	117,000	158,000	Use only largest quarter of brood years

Table 10: Sensitivity of SEG range based on ADFG Percentile Method to time period and rounding. Each cell in the table shows the SEG range in 1000s of Total Spawners, as well as the contrast in the data (c) and the resulting range of percentiles used to calculate the SEG according to the rules listed in Section 2.2.1)

Up To	Rounding Up	Rounding Up/Down	No Rounding
1999	44 – 130 (c = 3.9 / r = p15-Max)	43.8 – 98.8 (c = 4.1 / r = p15-p85)	43.56 - 127.49 (c = 3.9 / r = p15-Max)
2005	52.7 – 133 (c = 6.7 / r = p15-p85)	52 – 133 (c = 6.9 / r = p15-p85)	52.21 – 131.20 (c = 6.9 / r = p15-p85)
2013	56 – 130 (c = 6.7 / r = p15-p85)	55.9 – 130 (c = 6.9 / r = p15-p85)	55.68 – 127.67 (c = 6.8 / r = p15-p85)

Table 11: Point estimates of Linear Regression Ricker Parameters (MLE). Note that these SR fits are intended as a quick diagnostic check, and should not be used for setting spawning goals. Long-term smolt to adult survival rate is about 9%. DW = Durbin-Watson test of autocorrelation.

Data Set	a	σ_a	b	σ_b	Adj r^2	DW Stat	DW p value	Serial autocorrelation
Spn2Ad	4.31	1.24	8.26	2.08	0.40	0.73	0.00014	Very strong (<< 0.05)
Spn2AdAlt	4.53	1.24	8.64	2.07	0.43	0.86	0.00072	Very strong (<< 0.05)
Spn2Juv	32.8	1.26	5.38	2.14	0.21	0.76	0.00035	Very strong (<< 0.05)
FemSpn2Ad	4.26	1.22	8.04	1.86	0.44	0.79	0.00030	Very strong (<< 0.05)
FemSpn2AdAlt	4.39	1.22	8.26	1.87	0.46	0.88	0.00088	Very strong (<< 0.05)
FemSpn2Juv	33.8	1.25	5.62	1.92	0.27	0.86	0.00101	Strong (< 0.05)

Table 12: Biological Benchmark Estimates – Spn2Ad, Ricker Variations (MCMC). Benchmark estimates in 1,000s of total spawners, based on SR models fitted to total spawners and adult recruits estimated using age composition from the Canyon Island fishwheel data, using the code in Appendices B and C with OpenBUGS and the BRugs() function in R. These results are for all available years of data, capturing 1987 to 2009 brood years. S_{MAX}, S_{EQ}, and S_{MSY} are based on the equations in Table 5, including bias correction. p10 to p90 are percentiles of the posterior distribution (e.g. p25 means that 25% of the MCMC samples result in estimates below this number, and 75% of the MCMC samples result in larger BM estimates). The range from p10 to p90 captures 80% of the posterior distribution. p50 is the median. NPCV, SIQR, and SMAD are nonparametric measures of benchmark precision to summarize the spread of the posterior distributions (Section 2.5). For all three measures, a smaller value means higher precision. The shading in the middle column highlights the model-data combination identified as the most appropriate during the CSAS peer-review process, based on the rationale summarized in Section 5.1.2.

	Ricker		
Bench-mark	Basic	**AR1**	Kalman 2009 BY
S_{MAX}			
p10	98,000	82,000	94,000
p25	112,000	93,000	107,000
p50	**136,000**	**107,000**	**127,000**
p75	173,000	126,000	157,000
p90	247,000	154,000	244,000
NPCV	28%	18%	20%
SIQR	45%	31%	40%
SMAD	20%	15%	18%
S_{EQ}			
p10	167,000	158,000	126,000
p25	180,000	168000	138,000
p50	**201,000**	**183,000**	**150,000**
p75	233,000	202,000	171,000
p90	294,000	226,000	209,000
NPCV	16%	11%	13%
SIQR	27%	18%	22%
SMAD	12%	9%	10%
S_{MSY}			
p10	64,000	59,000	52,000
p25	70,000	63,000	57,000
p50	**79,000**	**69,000**	**62,000**
p75	94,000	77,000	71,000
p90	123,000	89,000	90,000
NPCV	18%	12%	14%
SIQR	30%	20%	23%
SMAD	14%	10%	11%

Table 13: Summary Reference Points (SRP) for Taku Coho – Alternative SR Models and Data Sets (MCMC). The reported Deviance Information Criterion (DIC) is total DIC from OpenBUGS output. ΔDIC = DIC –min(DIC). NPCV is a non-parametric coefficient of variation and proposed SRP are intended to summarize reference points used in recent ADFG and DFO reports (definitions in Section 2.5). All numbers in 1,000 Spawners. Female spawners are converted to total spawners based on long-term average of 40% females (Table A 1). Empty cells in PGY90 indicate that yield profile never exceeds 90% (it still has a clear peak, jut doesn't meet the 90% cut-off. See Figure 13). Empty cells for UBM90 are due to nonsensical values in the millions, because posteriors are very wide. Min and max for each column excludes the rows for Juvenile data sets. Figure 24 compares these SRP to the observed time series of spawner abundance. The shading in the second row highlights the model-data combination identified as the most appropriate during the CSAS peer-review process, based on the rationale summarized in Section 5.1.2.

						WSP		PGY90		60% Prob of		
Data Set	**SR Model**	**DIC (Fit)**	**ΔDIC**	**NPCV (S_{MSY})**	**SMSY50**	**LBM90**	**UBM90**	**L**	**H**	**70% MSY**	**80% MSY**	**90% MSY**
Spn2Ad	Ricker	-53	52	18%	79	32	98	55	98	35-123	44-112	57-98
-	**R. AR1**	**-55**	**50**	**12%**	**69**	**23**	**71**	**51**	**82**	**30-110**	**38-99**	**51-84**
-	Ricker K*	-97	8	14%	62	34	72	--	--	30-101	39-89	53-72
Spn2AltAd	Ricker	-53	52	16%	76	29	88	53	98	34-120	42-109	55-94
-	Ricker AR1	-50	55	23%	81	34	106	69	86	37-124	46-113	60-96
-	Ricker K*	-90	15	20%	64	40	102	--	--	32-99	41-86	--
Spn2Juv	Ricker	+38	143	145%	292	NA***	--	--	--	118-329	168-316	--
-	Ricker AR1	+22	127	37%	119	NA***	231	71	165	53-228	67-199	87-166
-	Ricker K**	+8	113	19%	96	NA***	111	61	157	42-191	53-167	70-139
FemSpn2Ad	Ricker	-53	52	14%	79	30	87	51	100	35-124	44-112	57-97
-	Ricker AR1	-53	52	13%	75	29	80	57	89	33-119	41-108	55-91
-	Ricker K*	-105	**0**	10%	59	28	57	--	--	29-96	36-86	50-71
FemSpn2AltAd	Ricker	-53	52	15%	79	30	86	54	101	34-124	43-113	57-96
-	Ricker AR1	-50	55	17%	81	33	93	64	87	36-124	45-113	59-96
-	Ricker K*	-99	6	17%	64	38	72	--	--	31-98	40-89	58-70
FemSpn2Juv	Ricker	+34	139	78%	237	NA***	--	124	185	99-349	126-316	175-242
-	Ricker AR1	+52	157	31%	124	NA***	199	72	178	55-242	69-212	91-178
-	Ricker K**	+10	115	18%	100	NA***	114	68	156	44-193	56-168	74-139
Min (Adult)	-	-105	0	10%	59	23	57	51	82	-	-	-
Max (Adult)	-	-50	157	23%	81	40	106	71	101	-	-	-
%Diff (Adult)	-	-	-	-	37%	74%	100%	39%	23%	-	-	-

* 2009 BY ** 2010 BY *** LBM90 not applicable to smolts (would require smolt to adult calculation)

Table 14: Sensitivity of S_{MSY} Estimates to alternative calculation methods – Spn2Ad. Derived S_{MSY} estimates use the equations in Table 5. Calculated S_{MSY} is the spawner abundance with largest median difference between recruits and spawners for 500 increments over the range [0,1.5 largest observed Spn]. MCMC are results from Bayesian fits using Markov Chain Monte Carlo methods (Section 2.3.3). MLE+B are results for maximum likelihood estimates of a simple regression on the linear form of the basic Ricker model combined with bootstrap distribution (Section 2.3.2). H&O is the software toolkit developed by Holt and Ogden (2013). All estimates rounded to the nearest 1,000 spawners. Point estimates are only available for the regression-based estimates, using point estimates of Ricker parameters. Percentiles summarize either the posterior distribution of MCMC samples or the bootstrap distribution for regression-based estimates.*

							Percentiles				
Row	**Model**	**Class**	**Method**	**R Pack**	**BM Var**	**Point Estimate**	**p10**	**p25**	**p50 (Median)**	**p75**	**p90**
1	Ricker	Derived	MCMC	BRugs	Corr	--	64	70	**79**	94	123
2	Ricker	Derived	MCMC	BRugs	Raw	--	61	67	**75**	88	112
3	Ricker	Derived	MCMC	r2JAGS	Corr	--	64	70	**78**	93	119
4	Ricker	Derived	MCMC	r2JAGS	Raw	--	61	67	**74**	87	108
5	Ricker	Derived	MLE+B	lm()	Corr	74	63	69	**77**	88	99
6	Ricker	Derived	MLE+B	lm()	Raw	70	59	64	**71**	79	89
7	Ricker	Derived	MLE	H&O	--	70	--	--	--	--	--
8	Ricker	Derived	MCMC	H&O	--	--	64	67	**72**	78	86
9	Ricker	Calculated	MCMC	BRugs	--	76	--	--	--	--	--
10	Ricker AR1	Derived	MCMC	BRugs	Corr	--	59	63	**69**	77	89
11	Ricker AR1	Derived	MCMC	BRugs	Raw	--	55	60	**66**	73	84
				Min (Ricker)		70	59	64	71	79	86
				Max (Ricker)		76	64	70	79	94	123
				% Diff (Ricker)		8%	8%	9%	11%	19%	43%
				Min (All)		70	55	60	66	73	84
				Max (All)		76	64	70	79	94	123
				% Diff (All)		8%	16%	17%	20%	29%	46%

Table 15: Range and precision of S_{MSY} estimates from Boostrap and MCMC fits – Spn2Smolt. Ranges are the 25th and 75th percentile of the bootstrap or MCMC sample. Precision is the non-parametric coefficient of variation (NPCV), as described in Section 2.5. A smaller NPCV means a narrower distribution (i.e. a more precise benchmark estimate). S_{MSY} values include bias correction (see Table 5). k=Thousands. M=Millions.

	Regression & Boostrap (MLE+B)		**Bayesian MCMC**	
SR Model	1990 to 2001 BY	1990 to 2010 BY	1990 to 2001 BY	1990 to 2010 BY
Ricker	47k – 74k (27%)	130k – 204k (33%)	59k – 214k (81%)	171k to 1.1M (145%)
Ricker AR1	--	--	38k to 86k (44%)	94k to 168k (37%)
Ricker Kalman (Last BY)	--	--	46k to 78k (31%)	84k to 114k (19%)

Table 16: Sensitivity of Yield-based Reference Ranges to Alternative Definitions. PGY ranges are numerical values corresponding to yield profiles based on overall median S_{MSY}. To create these profiles compare yield for different spawner levels to x% of MSY for overall median S_{MSY}, then check the % that is larger (i.e. OY-90-70 is the optimum yield range based on 90% probability of 70% of MSY). OY ranges are numerical values corresponding to ADFG-type yield profiles. To create these profiles compare yield for different spawner levels to x% of MSY for that parameter sample, then check the % that is larger (i.e. OY-90-70 is the optimum yield range based on 90% probability of 70% of MSY). All values in 1,000 Spn. Figure 15 shows the underlying yield profiles. Blank cells indicate that the yield profile doesn't reach the probability cut-off at any spawner abundance (see top two panels of Figure 15).

Criteria %Prob of % MSY	**SR Model**	**PGY**	**ADFG OY**
90-70	Ricker AR1	51-82	35-98
90-70	Ricker	55-98	48-105
90-80	Ricker AR1	-	43-89
90-80	Ricker	-	59-95
90-90	Ricker AR1	-	54-78
90-90	Ricker	-	75-81
60-70	Ricker AR1	30-110	28-111
60-70	Ricker	35-123	33-123
60-80	Ricker AR1	38-99	35-101
60-80	Ricker	44-112	41-112
60-90	Ricker AR1	51-84	44-89
60-90	Ricker	57-98	51-99

9. FIGURES

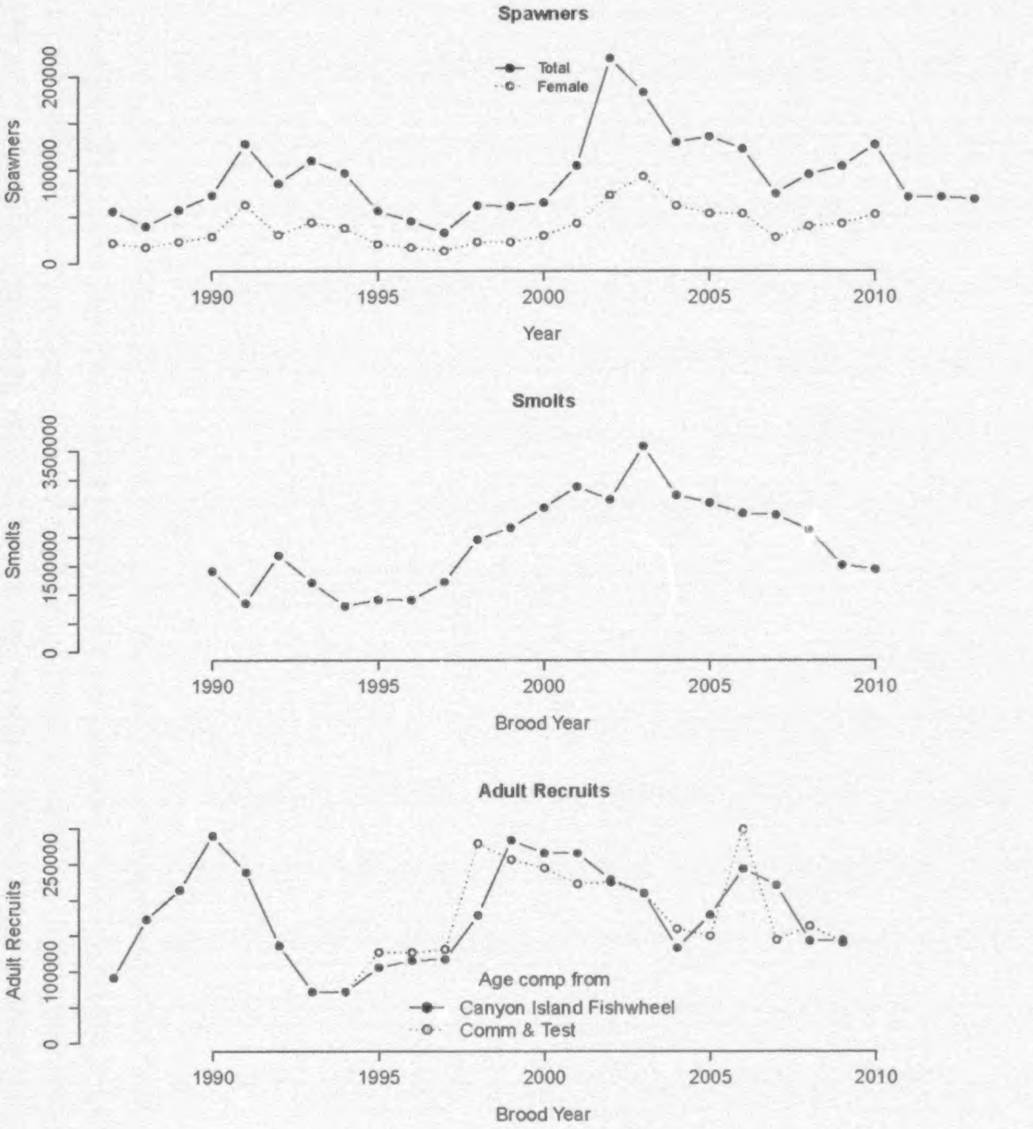


Figure 1: Abundance time series of spawners, smolts, and recruits by brood year for the Taku Coho stock aggregate. Consistent estimates of spawner abundance are available from 1987 to 2013, based on a mark-recapture survey. Trapping-based smolt estimates are available for brood years 1990 to 2010. Adult recruit estimates are available for brood years 1987 to 2009, derived from annual estimates of spawner abundance and catch based on age composition. Two alternative age composition data sets are available, resulting in alternative recruit time series. Data sources are summarized in Section 2.1.1. Table A 1 lists the values shown in this figure.

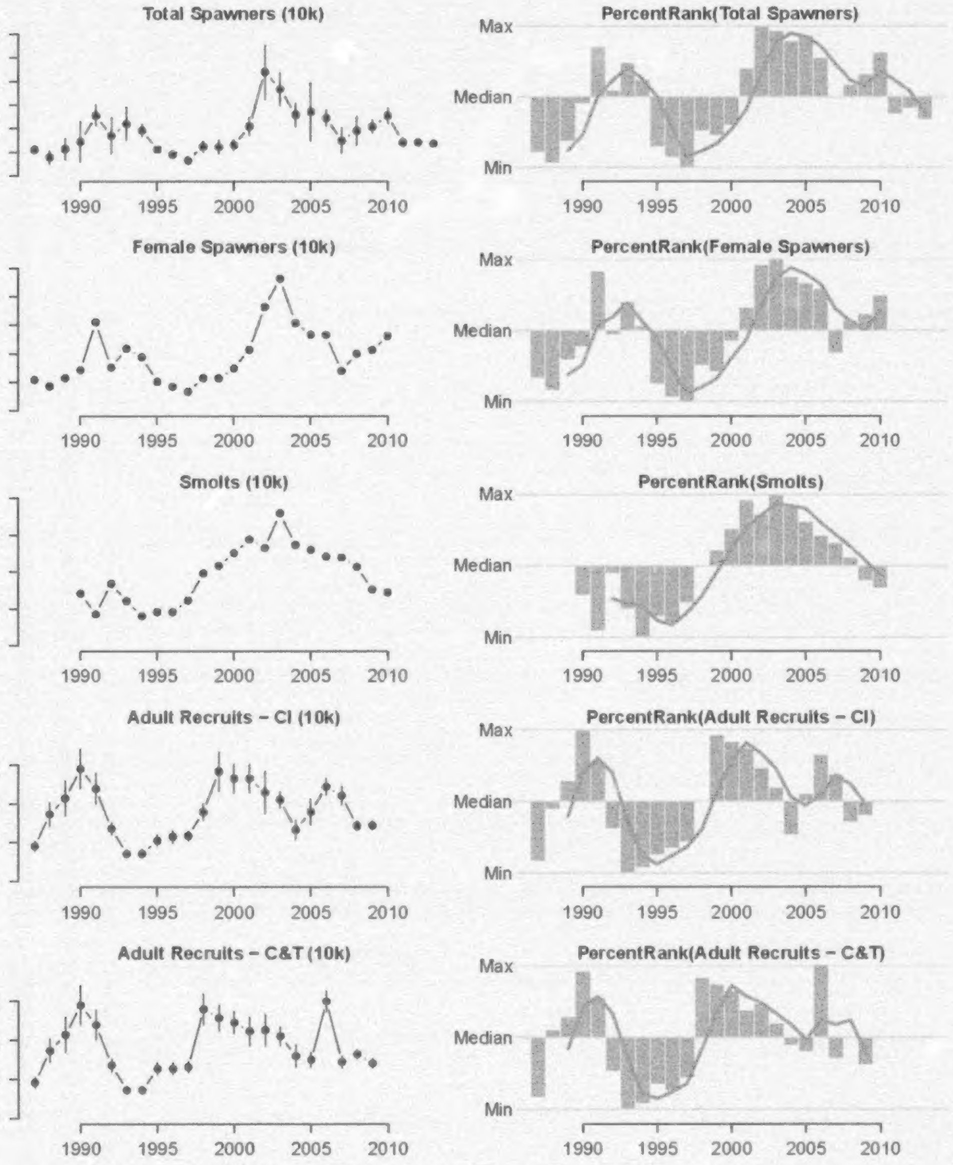
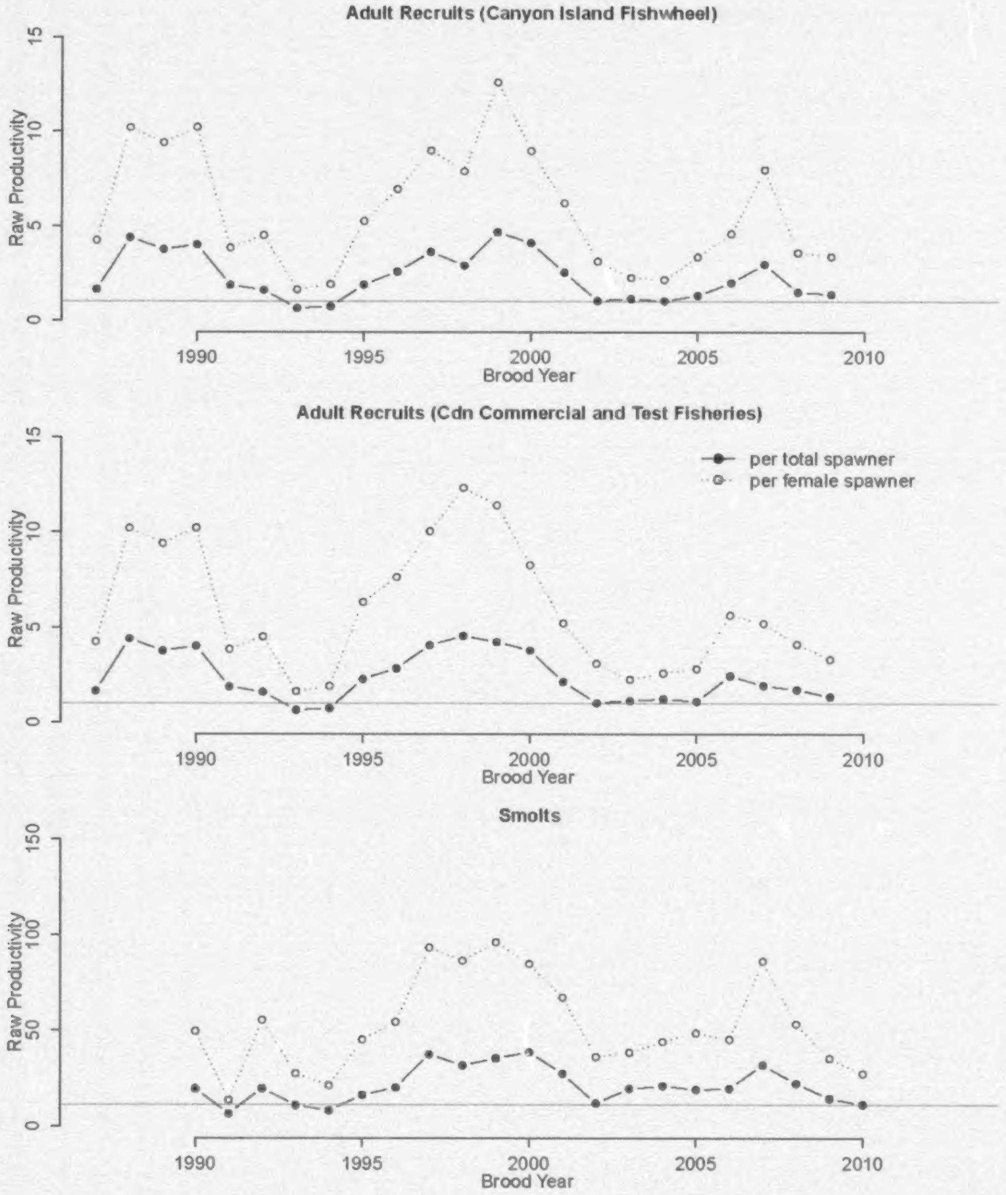


Figure 2: Observation error and rescaled patterns in time series of spawners, smolts, and recruits by brood year for the Taku Coho stock aggregate. Panels on the left show the same time series as Figure 1, with the addition of errors bars covering ± 2 standard errors for each observation. All values in 10,000 fish. The panels on the right show the matching time series rescaled as ranked deviations from the median as a barplot with 4-yr running average as a red line. Percent rank calculations are documented in Section 12.1.


Adult Recruits (Canyon Island Fishwheel)

Adult Recruits (Cdn Commercial and Test Fisheries)

Smolts

Figure 3: Raw productivity patterns for the Taku Coho stock aggregate. Raw productivity is defined simply as the ratio of offspring/parent without adjusting for abundance of parents. Data are the same as Figure 1. Horizontal lines mark the replacement level at 1 recruit per total spawner or 11.4 smolts per total spawner (based on long-term average smolt-to-recruit survival of 9%). Note that the replacement lines only apply to raw productivity for total spawners (i.e. solid lines, filled circles), and can't be compared to the raw productivity of female spawners (i.e. dashed lines, open circles).

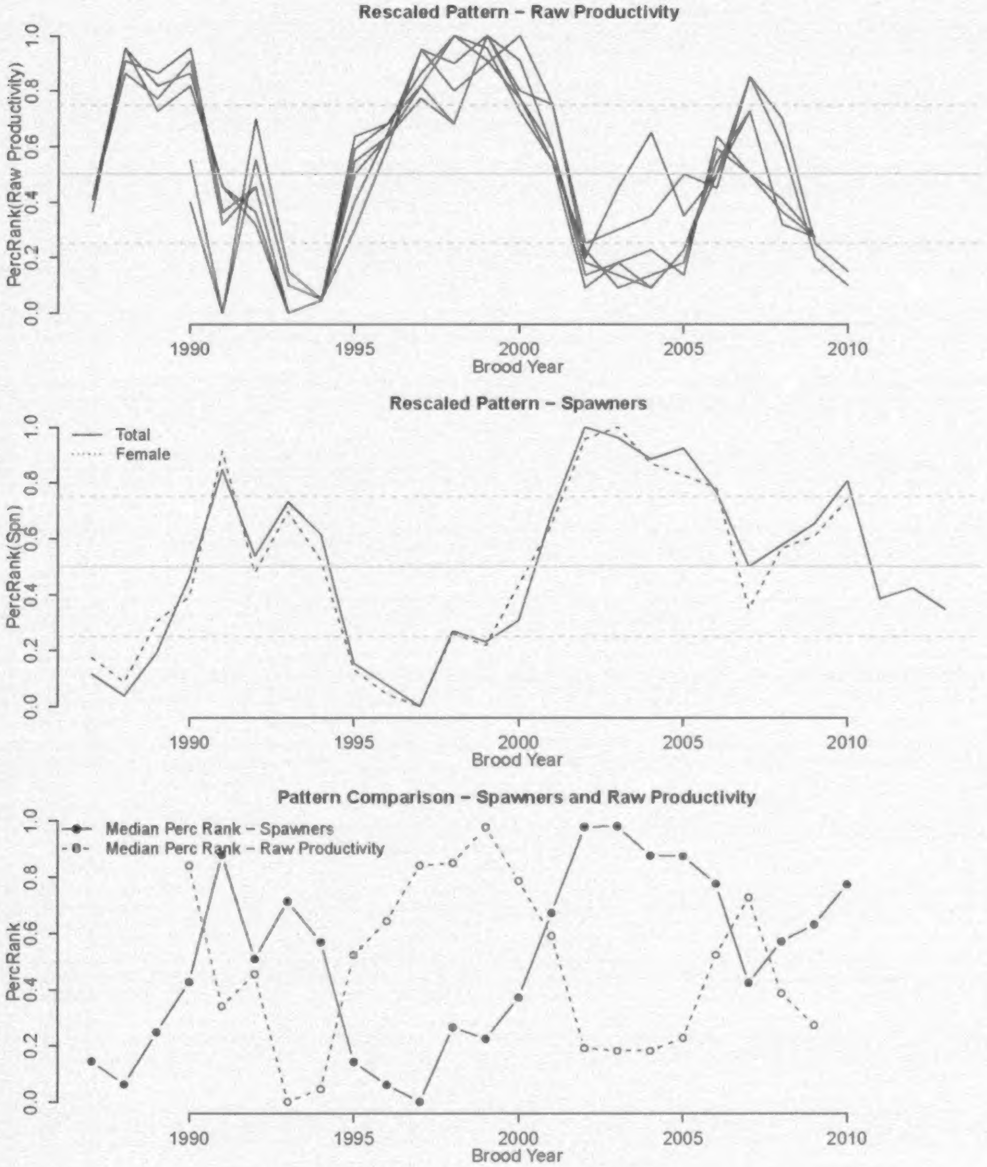


Figure 4: Rescaled patterns in abundance and raw productivity. The top panel shows the 6 time series of productivity from Figure 3 rescaled as percent ranks. The middle panel shows 2 alternative spawner timer series rescaled as percent ranks. The bottom panel compares the averaged time series from the top and middle panels. Percent rank calculations are documented in Section 12.1. Horizontal lines show the median (solid) and quartiles (dashed).

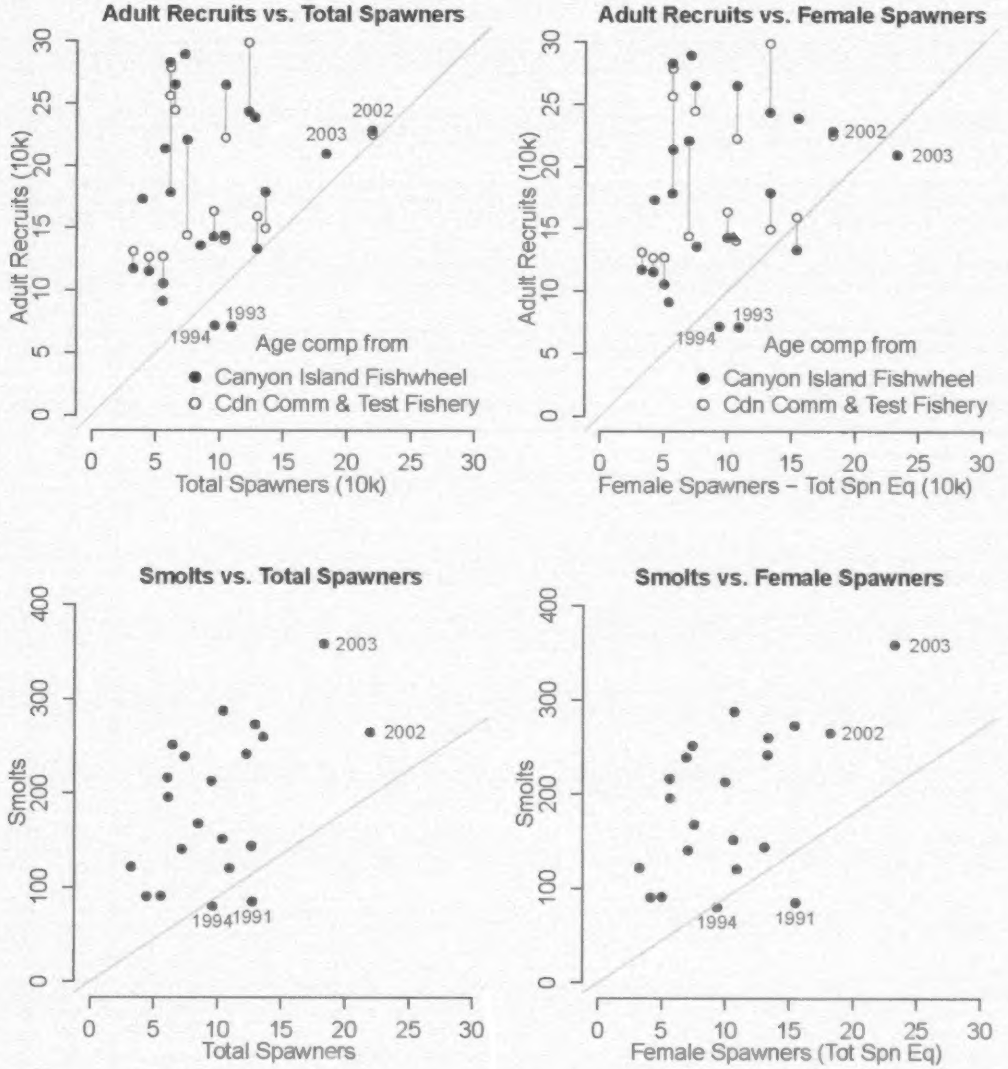


Figure 5: Pairwise plots of spawners, smolts, and recruits by brood year for the Taku Coho stock aggregate. The top panels show the effect of assumptions about age composition on the Recruit vs Spawner scatterplot, with solid points showing estimates based on the Canyon Island fishwheel data, and open circles showing the alternative recruits estimates based on age composition in the Canadian commercial and test fisheries. The red lines connect matching points. Female spawners are expanded to total spawner equivalents based on long-term sex-ratio of 40% females. Diagonal lines show replacement (i.e. recruits = spawners) in the top panels, and approximate replacement (11.4 smolts = spawners, based on long-term average smolt to adult survival of 8.8%) in the bottom panels. All values in 10,000 fish.

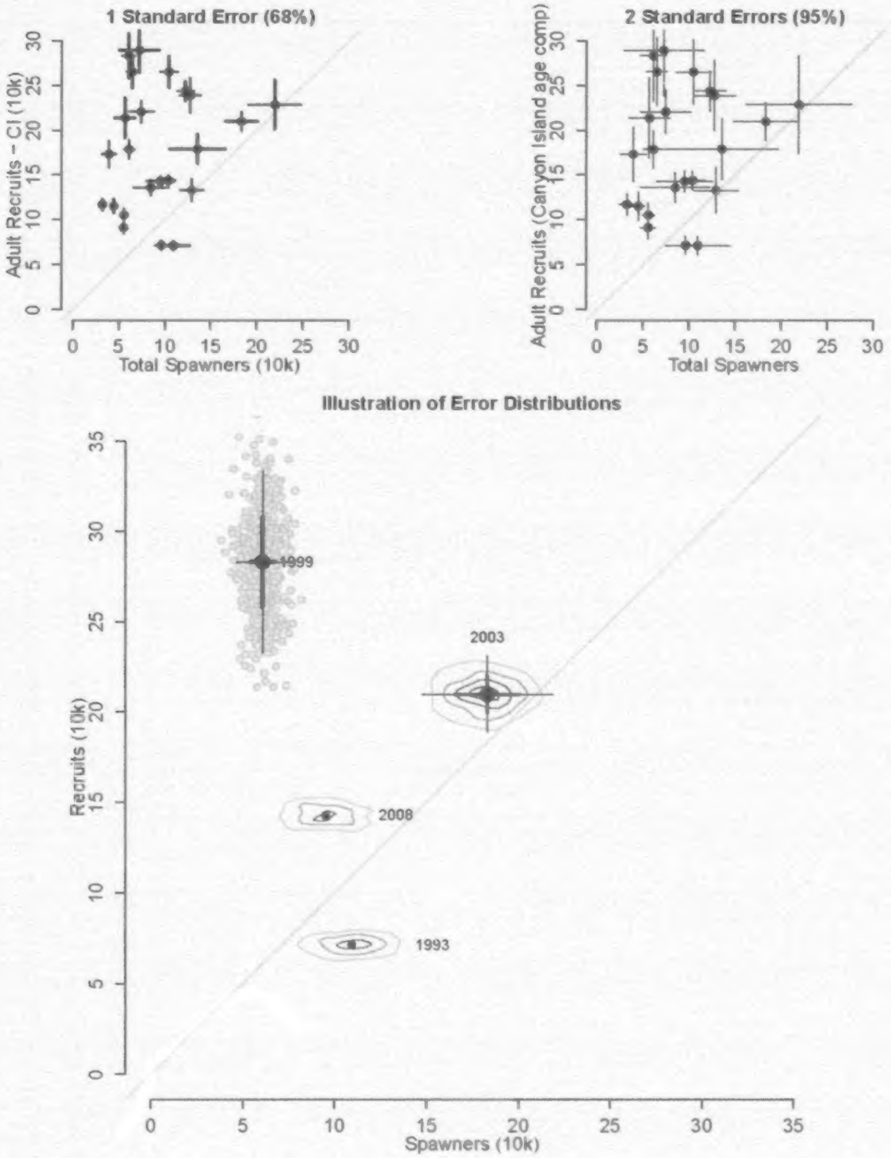


Figure 6: Observation error in estimates of spawners and recruits by brood year for the Taku Coho stock aggregate. Estimates of observation error are available for Taku River Coho Salmon spawner and recruit data (Section 2.1.1). The top two panels show bivariate error bars for 1 standard error, which captures 68% of each univariate distribution, and 2 standard errors, which captures 95% of each univariate distribution. The length of the cross-hairs indicates the range of values, but note that values near the center are more probable. The bottom panel illustrates the resulting bivariate scatter with 500 resampled values for 4 observations. Some data points are clearly more uncertain than most of the others (e.g. 2002 on the far right, 2005 near the middle), and data points can be more uncertain along one of the axes (e.g. 1999 has a vertical scatter indicating that the recruit estimate is more uncertain than the spawner estimate, 2008 shows the opposite pattern). Appendix Table A 2 lists the estimates and observation errors.

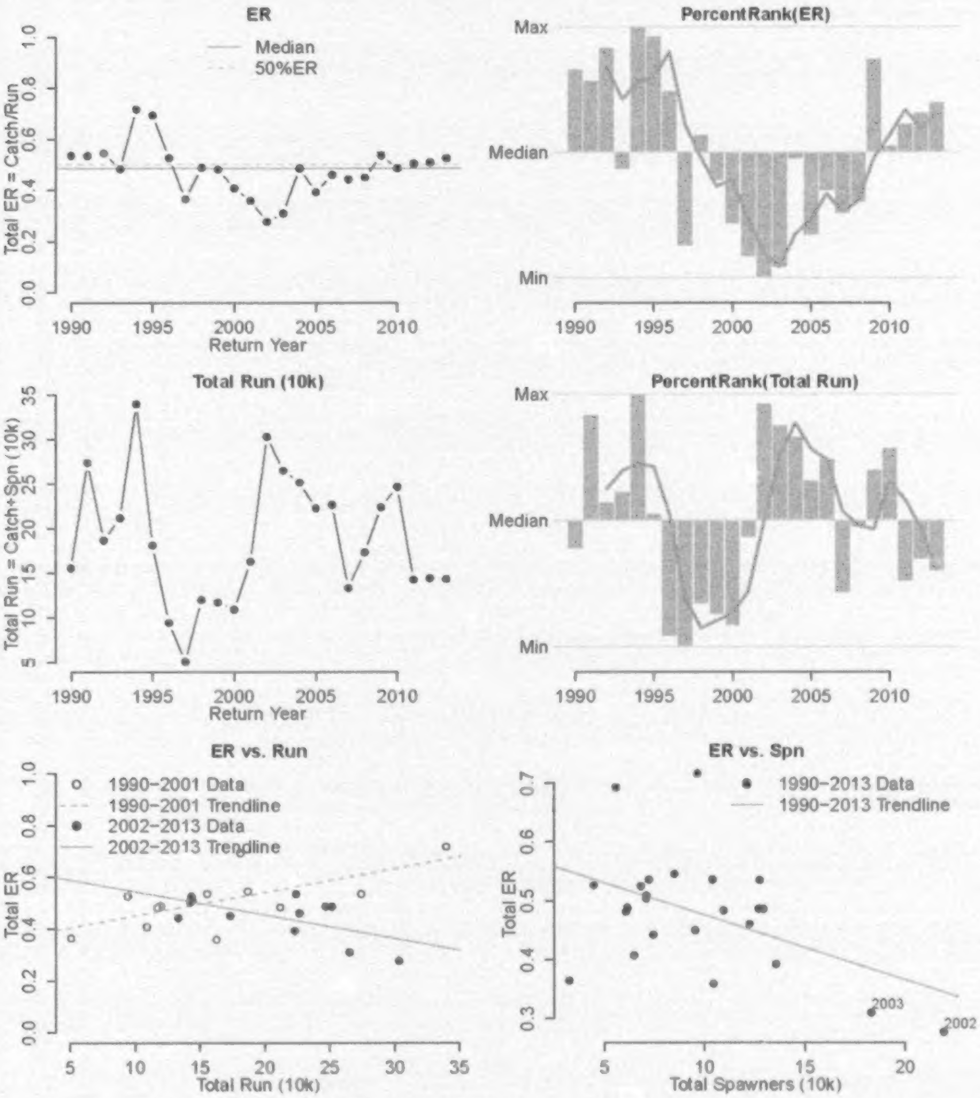


Figure 7: Overview of Taku Coho harvest patterns since 1990. The top 2 panels show the pattern in overall exploitation rate (ER) over time. The left panel shows the estimates, and the panel on the right show the matching time series rescaled as ranked deviations from the median as a barplot with 4-yr running average as a red line. The middle panels show total run in the same format. The bottom panel shows how ER has changed with abundance in 2 time periods. Trendlines are simple linear regressions. Data sources are summarized in Section 2.1.1, with details documented in Appendix A. Percent rank calculations are documented in Section 12.1.

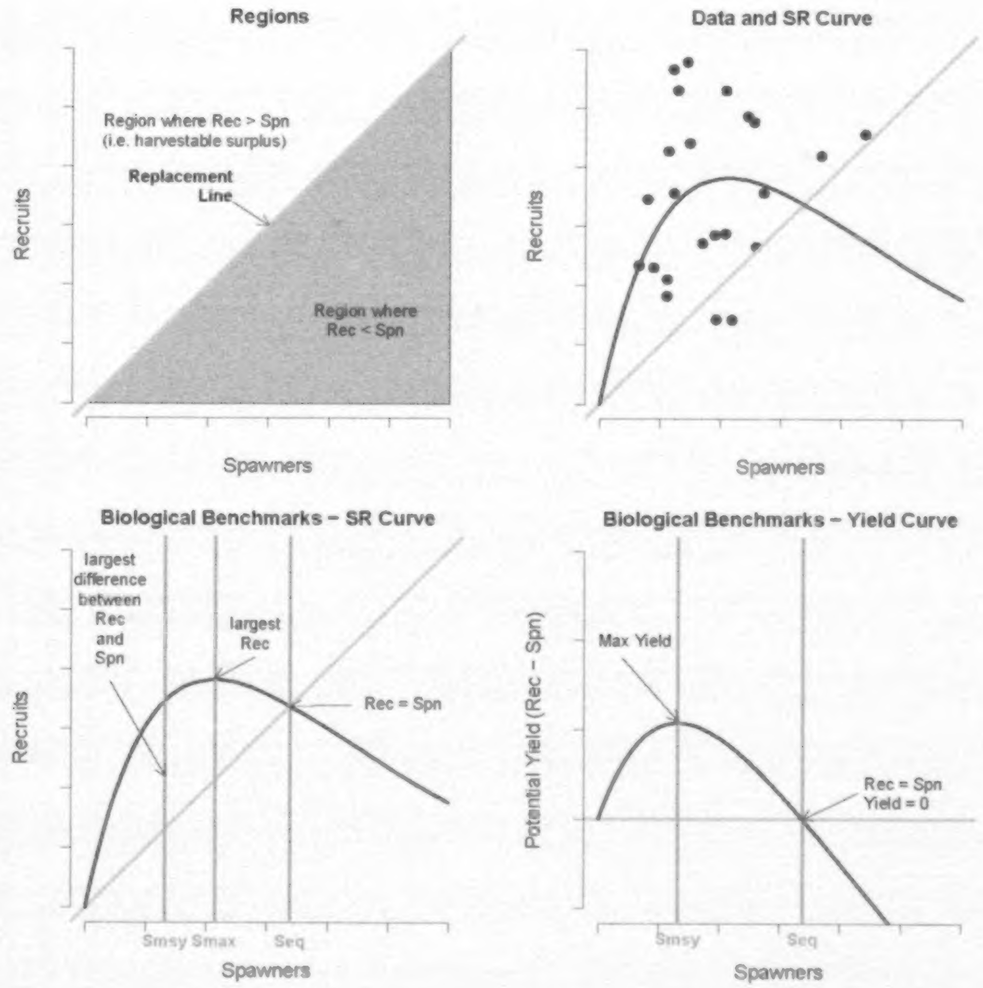


Figure 8: Graphical Illustration of Biological Benchmark Definitions. Biological benchmarks describe the estimated long-term average properties of the population, independent of the management approach. Table 1 defines the biological benchmarks illustrated in this figure. Section 1.3 and Table 4 summarize how these benchmarks are linked to Canada's Wild Salmon Policy and Alaska's Sustainable Salmon Policy.

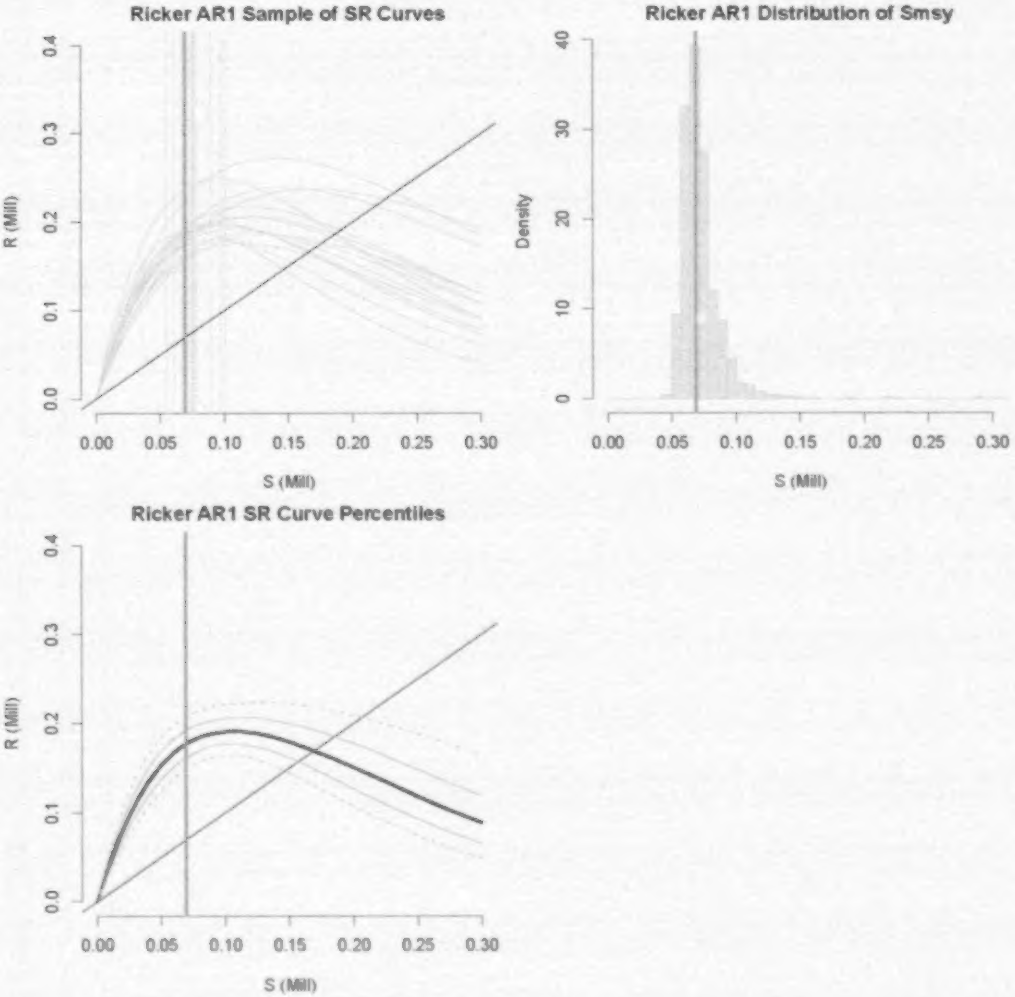


Figure 9: Illustration of uncertainty in spawner-recruit parameters and resulting uncertainty in estimates of S_{MSY}. All 3 panels show results for the Ricker AR1 model fitted to the Spn2Ad dataset. The vertical red line in all 3 panels marks the overall median estimate of S_{MSY}, labeled SMSY50 throughout the document. The diagonal line in Panels A and C is the replacement line with 1 recruit/spawner. Panel A shows a random subsample of 15 Ricker curves from the 2000 parameter sets sampled from the posterior distribution with vertical lines marking the corresponding S_{MSY} estimates for each curve. Panel B shows the distribution of all 2000 S_{MSY} estimates sampled from the posterior distribution. Panel C shows the median Ricker curve and percentile envelopes capturing 50% and 80% of the 2000 Ricker curves (i.e. 25th to 75th percentile, 10th to 90th percentile). Subsequent calculations can be based on either one of these 3 variations. For example, the alternative yield profiles in Figure 15 are based either on comparisons to the median Ricker curve in Panel C or comparisons to each of the individual curves illustrated in Panel A.

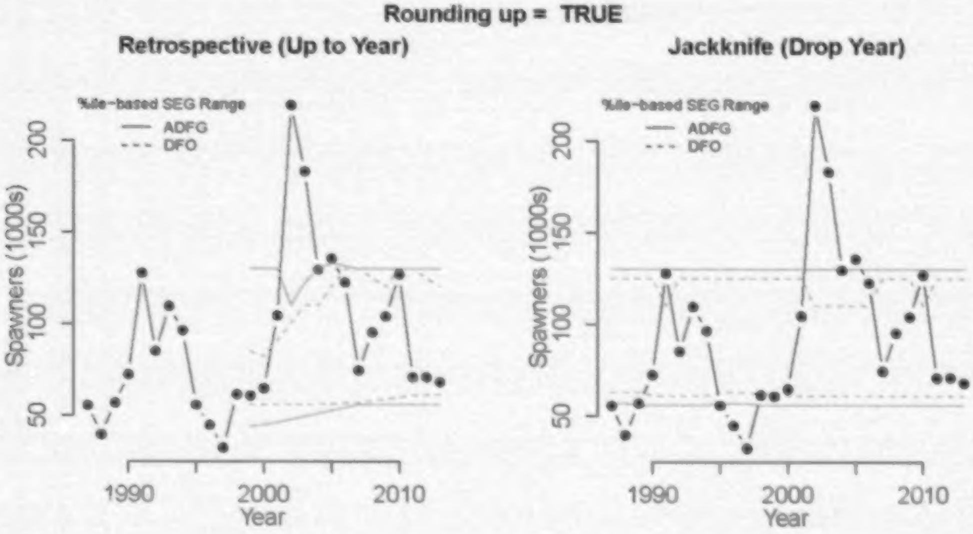


Figure 10: Sensitivity analysis of SEG range based on Percentile Method. Both panels show the time series of spawners for Taku coho and the estimated range for the Sustainable Escapement Goal (SEG) based on observed percentiles (Section 2.2.1). Left panel shows the change in SEG over time as additional observations are added. Right panel shows effect of dropping individual observations. The SEG range is wide, but highly stable over time.

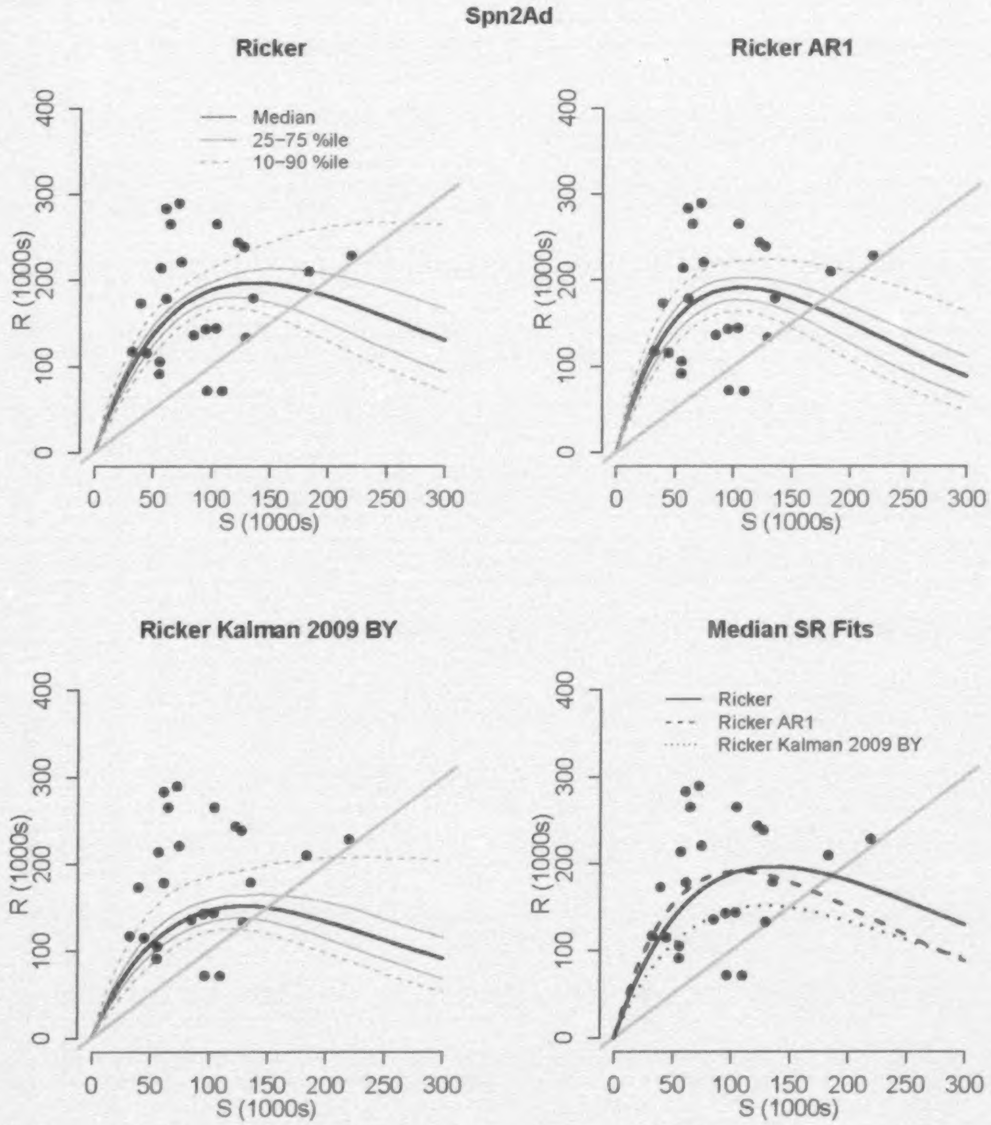


Figure 11: Spn2Ad Ricker Variations – SR Fits. Each panel shows observed recruits (R) and spawners (S) for the spawner to adult base-case data set (Spn2Ad), with adult recruit estimates based on age composition in the Canyon Island fishwheel samples (i.e. solid points in top left panel of Figure 5. Curves show the distribution of fitted values (i.e. distribution of recruitments calculated for each MCMC parameter sample) for 3 variations of the Ricker model. Diagonal lines show replacement (i.e. recruits = spawners). The bottom right panel compares median curves for the 3 alternative model types.

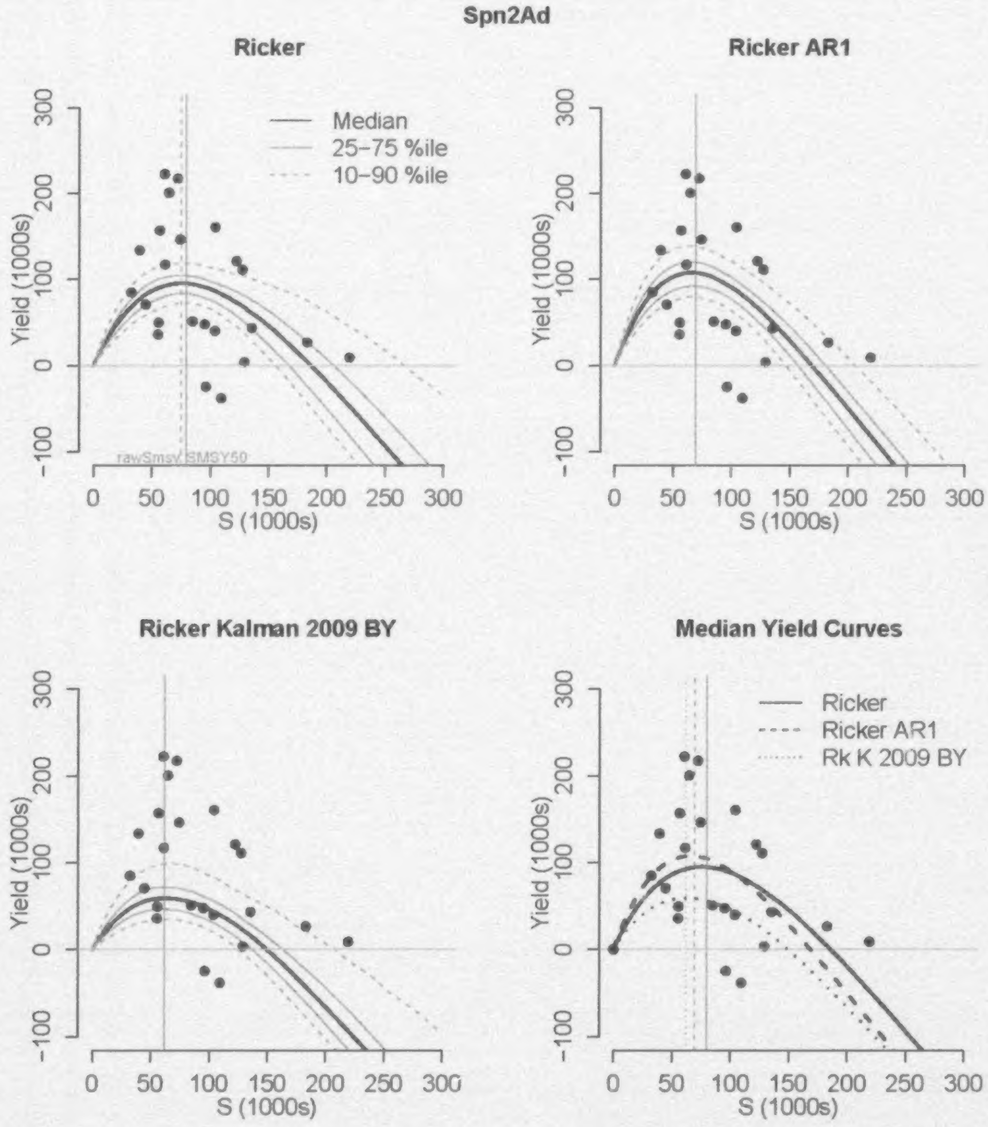


Figure 12: Spn2Ad Ricker Variations – Yield Curve. Each panel corresponds to the SR curves in Figure 11, except that the vertical axis is yield, calculated as recruits – spawners (R-S). Horizontal lines show replacement (i.e. recruits = spawners; yield = 0). Vertical lines show estimates of S_{MSY}. The first panel compares median S_{MSY} without bias correction (rawSmsy) and with bias correction (SMSY50). Subsequent panels show only SMSY50 estimates. The final panel compares SMSY50 estimates for the 3 alternative model forms. For benchmark descriptions, refer to Section 2.3.4, Section 2.5, and Table 5.

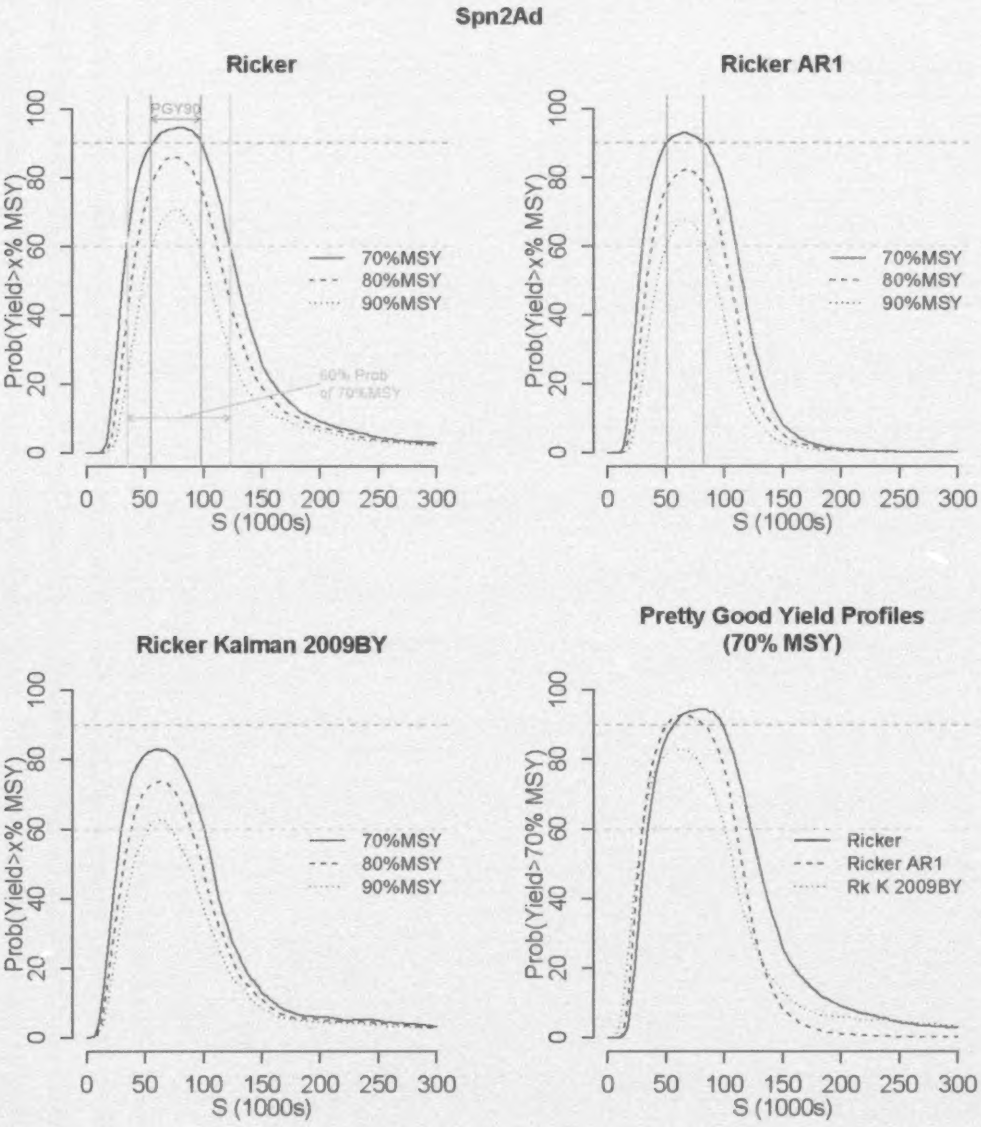


Figure 13: Spn2Ad Ricker Variations – Pretty Good Yield Profile. Each panel corresponds to the yield curves in Figure 12, except that the distribution of yields at each spawner level is expressed as the proportion of samples where yield exceeds 70%, 80%, or 90% of MSY (i.e. median yield at median S_{MSY}). PGY90 is the range where more than 90% of the parameter samples produce yields larger than 70% MSY. An alternative reference range, which spans a wider range of spawner abundances, is based on 60% of the samples exceeding 70% MSY. These ranges are used in Table 13 to compare results across alternative models and data sets.

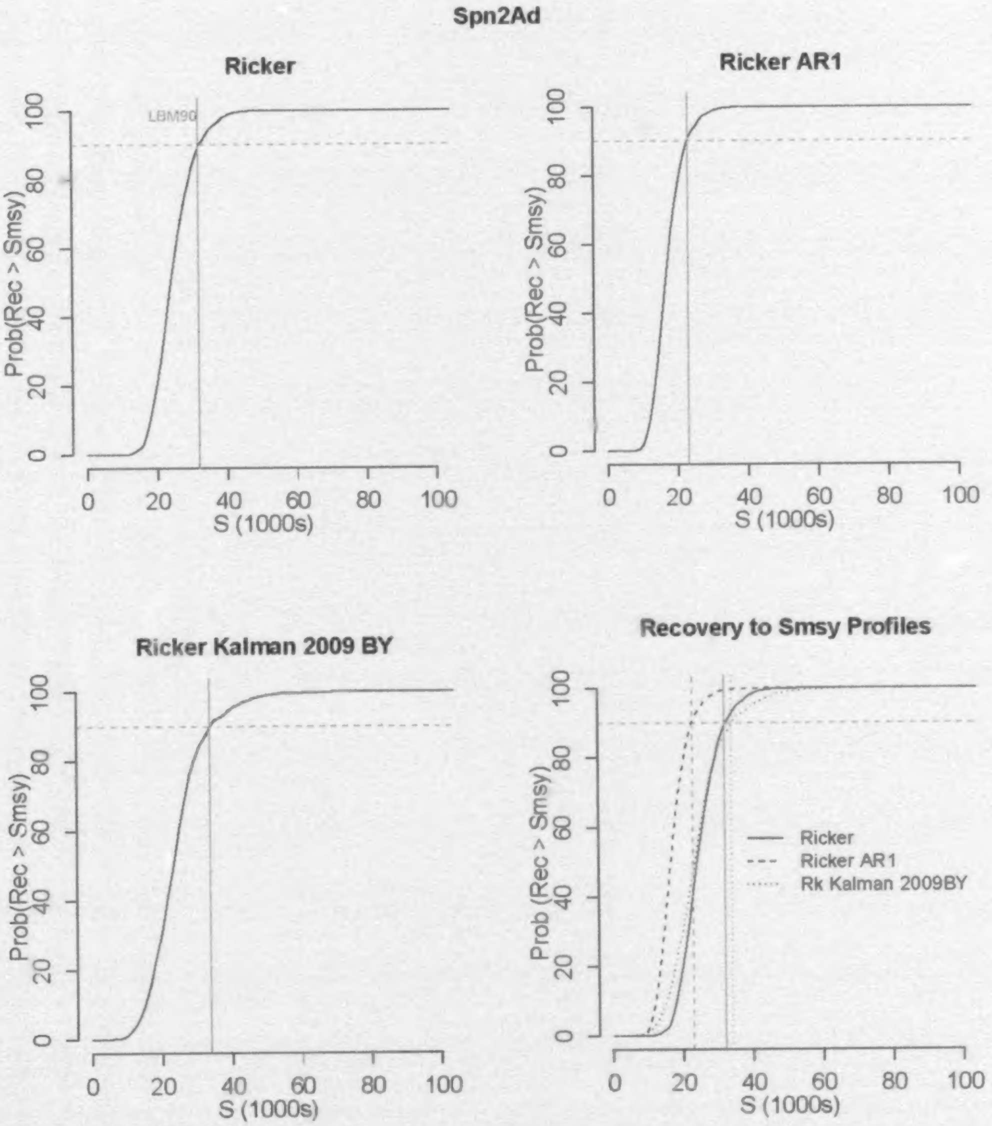


Figure 14: Spn2Ad Ricker Variations – Recovery Profile. Each panel corresponds to the SR curves in Figure 11, except that the distribution of recruits at each spawner level is expressed as the proportion of samples where recruits exceed median S_{MSY}, such that the stock aggregate would rebuild to S_{MSY} in 1 generation in the absence of fishing. The spawner abundance where the recovery profile crosses the 90% threshold is labeled as LBM90, and corresponds to the upper end of the distribution for $S_{gen.}$ which serves as the lower benchmark for Relative Abundance in status assessments under Canada's WSP.

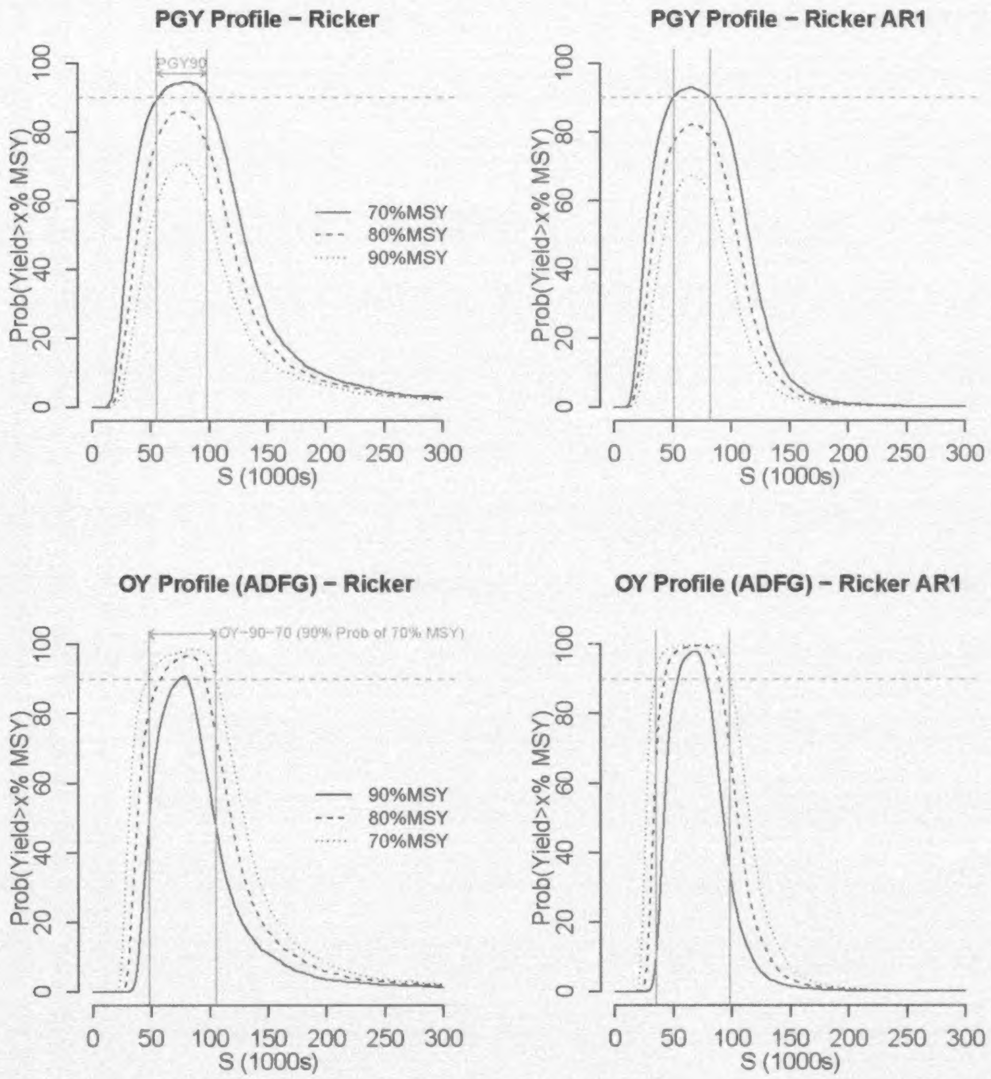


Figure 15: Alternative Reference Ranges – Pretty Good Yield vs ADFG-type Optimum Yield Profiles. The panels on the top show the probability of achieving 70, 80, or 90% of median MSY at the ***overall*** *median S_{MSY} (i.e. the yield profiles underlying the reference ranges in Table 13). The panels on the bottom show the probability of achieving 70, 80, or 90% of median MSY at median S_{MSY} estimate for each parameter set sampled from the posterior distribution (i.e. the yield profiles underlying the ADFG-type reference ranges). Table 16 lists the corresponding reference ranges. Figure 9 illustrates the source of the difference. The PGY profiles are based on comparison to the median SR curve in the bottom left panel of Figure 9, while the OY profiles are based on comparisons for each SR curve, with a small sample shown in the first panel of Figure 9.*

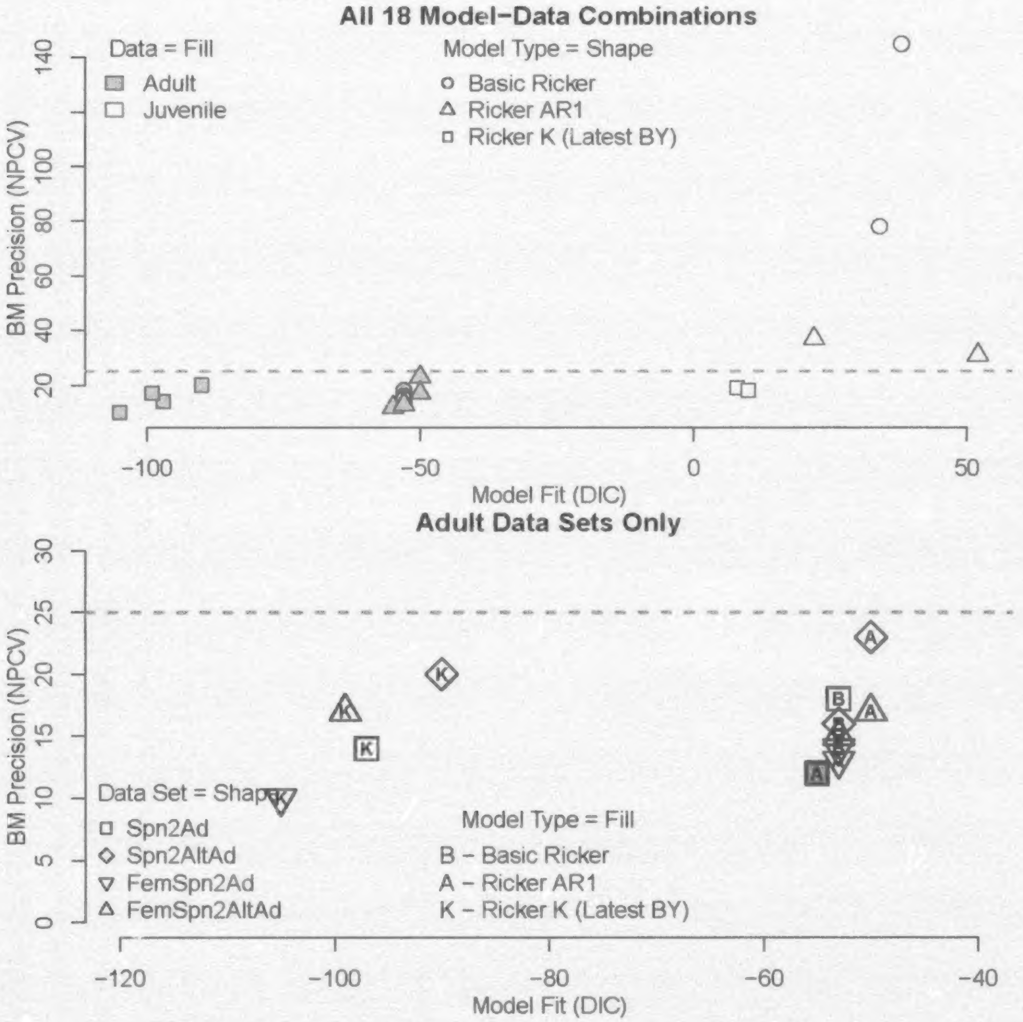


Figure 16: Model Fit vs. Benchmark Precision (DIC vs. NPCV). Each point in the figure corresponds to one of the 18 sensitivity analyses listed in Table 13 (6 data sets, 3 alternative SR models each). Model fits are expressed as the Deviance Information Criterion (DIC), which is the standard measure of fit for MCMC. Lower DIC values indicate better fit. Benchmark precision is expressed as the Non-Parametric Coefficient of Variation (NPCV) for the resulting S_{MSY} estimate, following the approach by Clark et al. (2009). Lower NPCV values indicate higher precision (i.e. narrower range). The top panel shows that models fitted to variations of adult data have a better fit (lower DIC). The bottom panel shows that the Ricker Kalman model fits better than the Basic Ricker or Ricker AR1. The CSAS-recommended model-data-combination (Ricker AR1 fitted to Spn2Ad data; see Section 5.1.2) is highlighted as the red-filled square plotting symbol in the bottom panel.

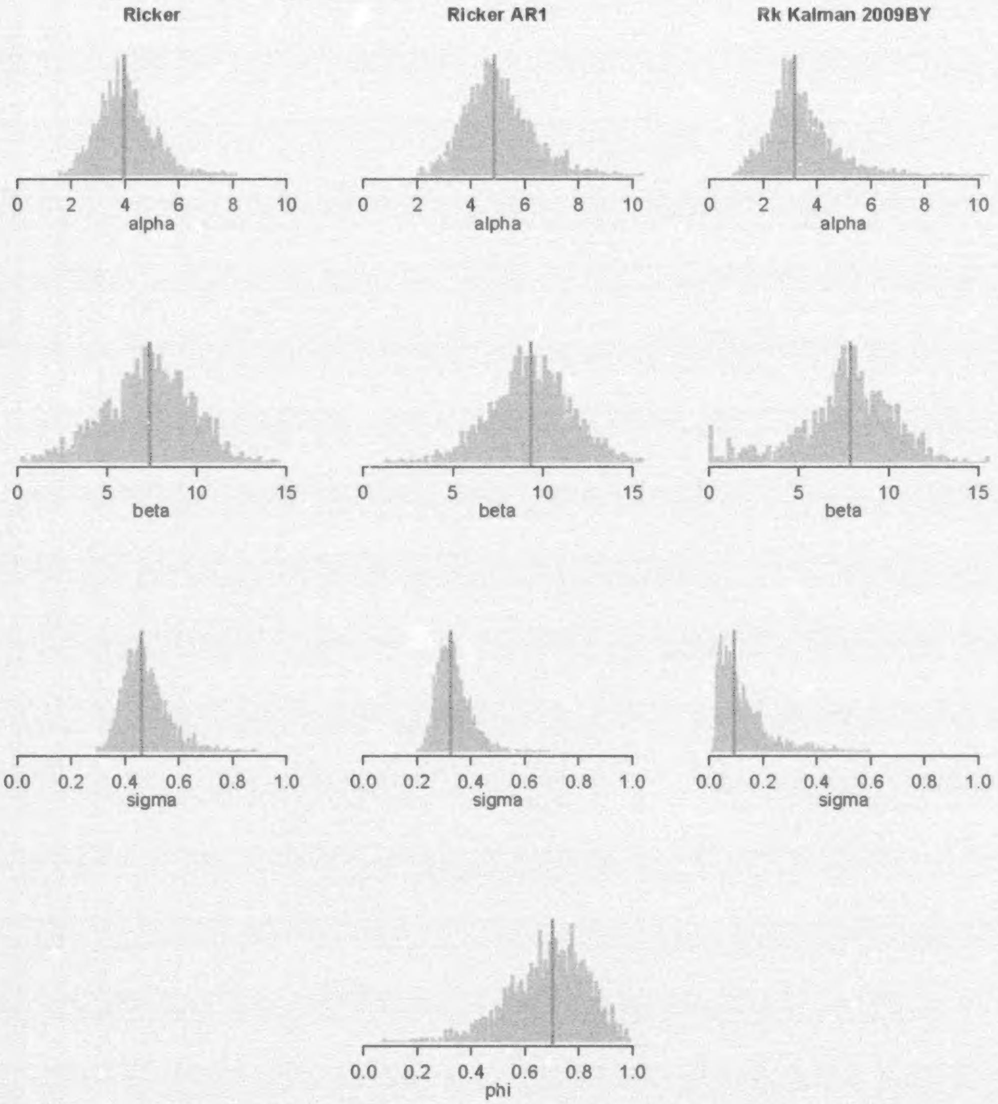


Figure 17: Posterior Distributions – 3 Ricker variations; Spn2Ad. Each panel shows a histogram of 2,000 parameter samples, thinned from 2 chains of 40,000 MCMC samples each. Vertical lines show the median for each parameter sample. Table 5 list parameter definitions.

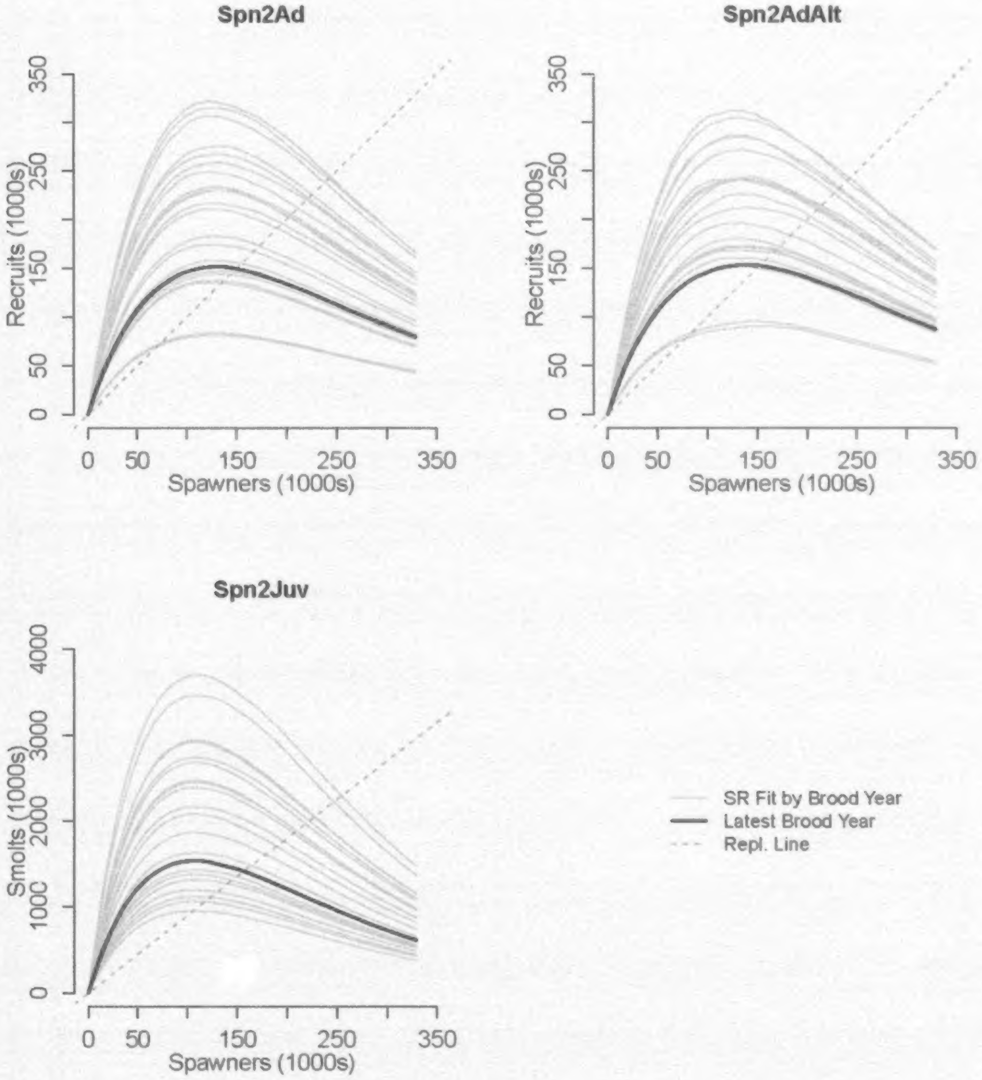


Figure 18: Median SR curve by Brood Year – Ricker Kalman. The Kalman-filtered Ricker model estimates an underlying pattern in productivity from the observed data (i.e. time-varying ***Error! Bookmark not defined.*** *α parameters). As a result, the Ricker curve shifts up and down over time. Each panel shows the median fit for different brood years (1987 to 2009 for adult recruits, 1990 to 2010 for smolts). The latest brood year is highlighted. Note that the location of peaks, corresponding to S_{MAX}, stays the same across brood years, but the intersect with the replacement line, corresponding to S_{Eq}, changes substantially. Figure 19 shows how S_{MSY} varies by brood year for each of these alternative SR curves. For both of the adult data sets, the Kalman fits clearly pick out the low productivity years (1993, 1994) as the two SR curves with the lowest peak (low productivity = low peak in this figure and low S_{MSY} in Figure 19)*

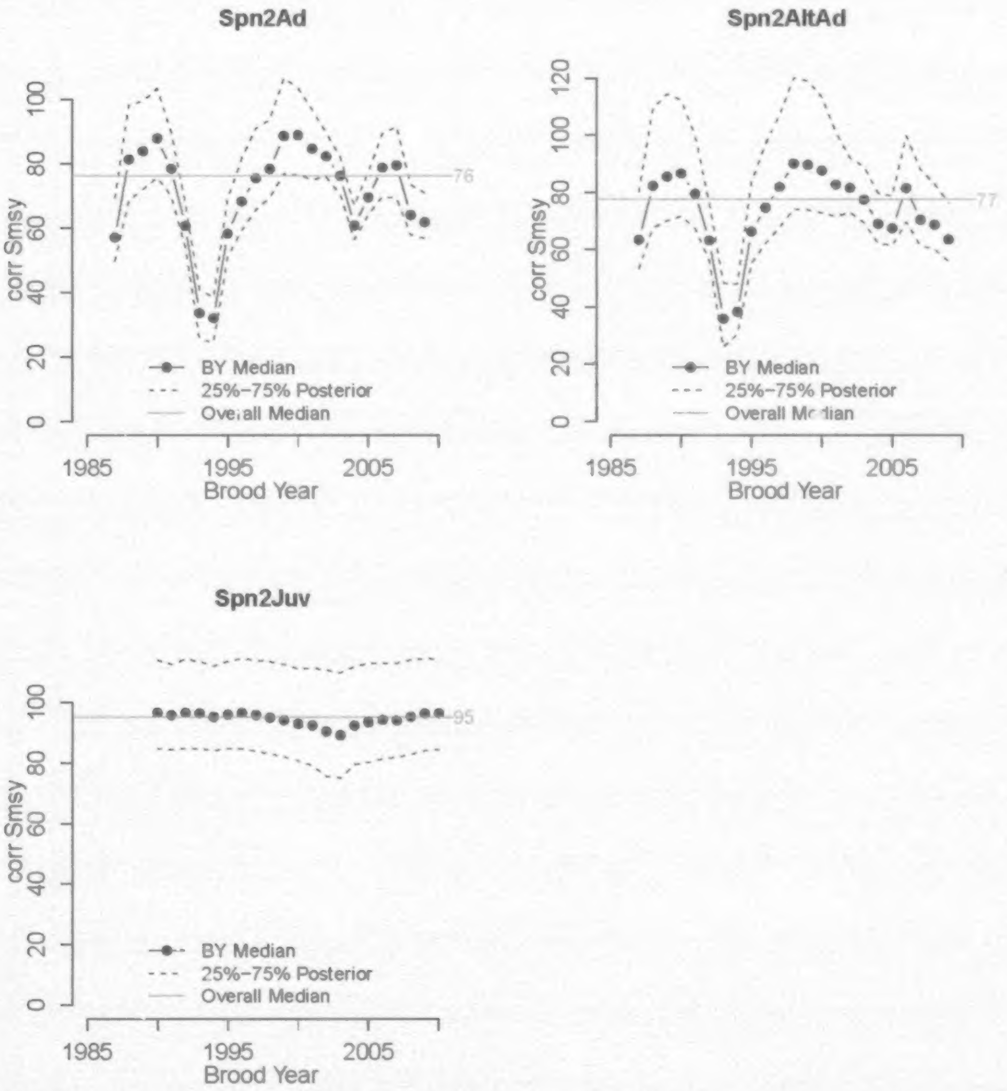


Figure 19: S_{MSY} range by Brood Year – Ricker Kalman. The Kalman-filtered Ricker model estimates an underlying pattern in productivity from the observed data (i.e. time-varying ***Error! Bookmark not defined.*** *α parameters). This figure shows the resulting variation in the estimated range of S_{MSY}. Each panel shows the pattern for the same SR model form, but estimated for 3 alternative data sets. All 3 data sets use total spawners, but recruitment data is either adult recruits based on age composition in the Canyon Island survey (Spn2Ad), adult recruits based on age composition in the Canadian commercial and test fishery (Spn2AltAd), or smolts (Spn2Juv).*

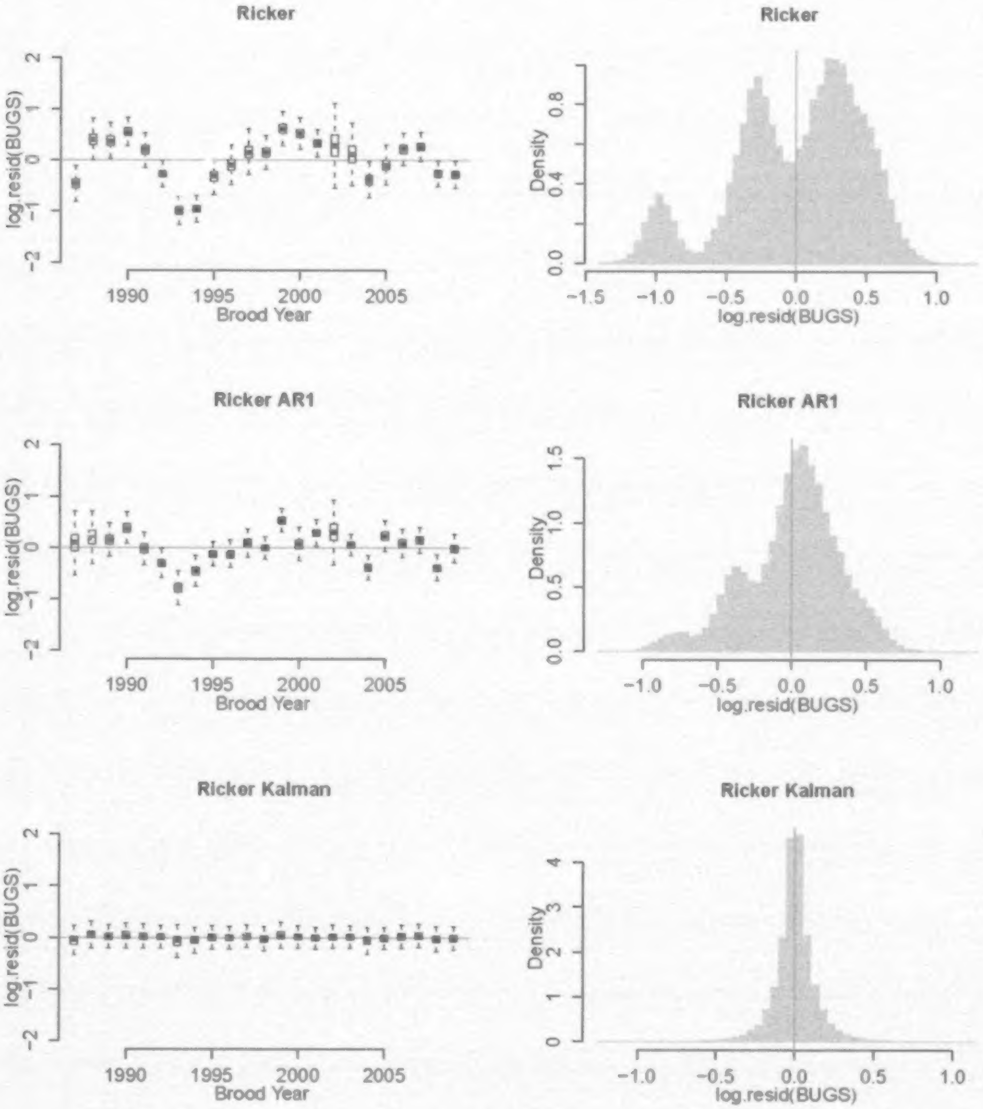


Figure 20: Residual patterns for 3 Ricker variations – Spn2Ad. Left panels show the residuals by brood year. Each boxplot captures standard percentile values (p10, p25, median, p75, p90) of log-residuals for 2,000 parameter samples, thinned from 2 chains of 40,000 MCMC samples each (i.e. each parameter sample gives a time series of Obs Rec – Fitted Rec). Right panels show the shape of the distribution of log-residuals across all brood years.

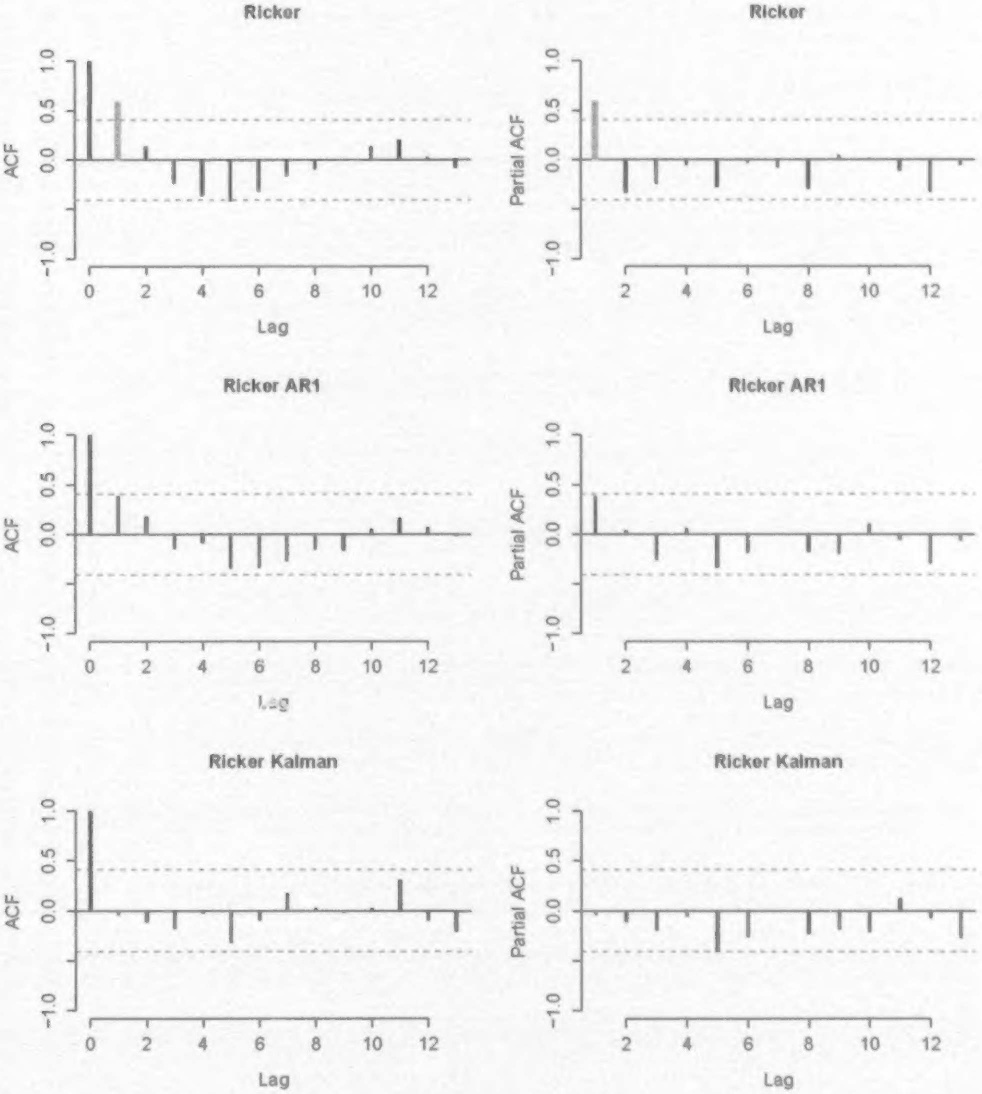


Figure 21: Residual autocorrelation patterns for 3 Ricker variations – Spn2Ad. All panels are based on the pattern in median log-transformed residuals for the 3 alternative model fits (i.e. mid-points of the boxplots in the left-hand panels of Figure 20). Panels on the left show the autocorrelation function (ACF) at lag t and panels on the right show partial autocorrelation left in the time series after accounting for ACF (i.e. to remove spurious patterns propagated by autocorrelation at lag t) . Horizontal dashed lines show 95% confidence intervals, such that any values outside the confidence band indicate significant autocorrelation. For example, if residuals are strongly correlated with the previous year's residuals, then the ACF and partial ACF would both be significant at lag 1. The ACF might also show autocorrelation at higher lags, but these are only real if confirmed in the partial ACF. Residuals from the basic Ricker model in the top row show strong lag 1 autocorrelation, but both the Ricker AR1 and Ricker Kalman models correct for this.

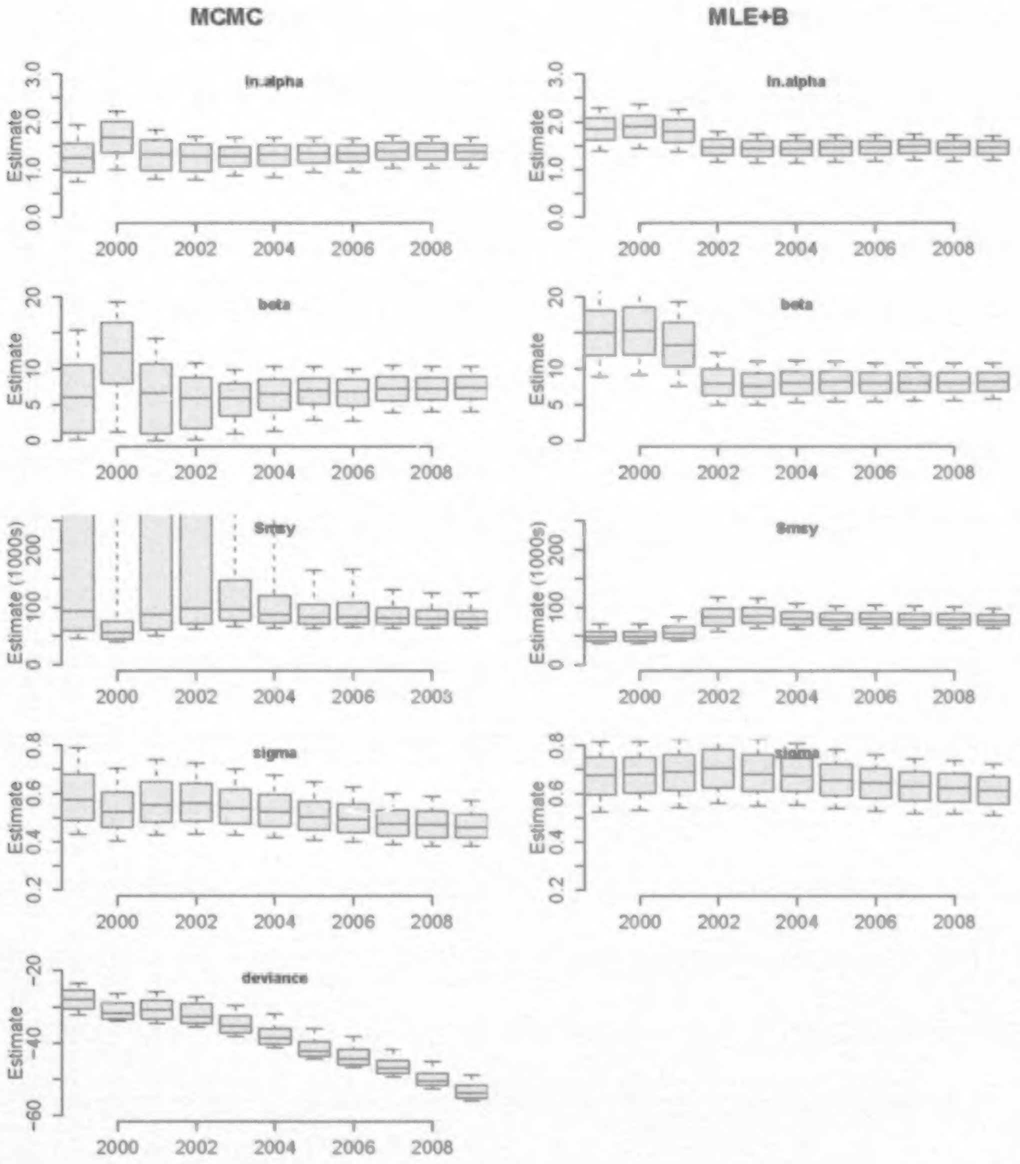


Figure 22: Retrospective Test of MLE+B vs MCMC - Ricker, Spn2Ad. All figures show the change in estimates as additional data are added, starting with model fits for the 1987-1999 brood years up to model fits for the 1987-2009 brood years. Left panels show estimates for the basic Ricker fit using Bayesian MCMC with BRugs and OpenBUGS. Right panels show fits for the same data set and model form, just using simple linear regression and bootstrapping. The horizontal axes identify the last brood year used in the data set.

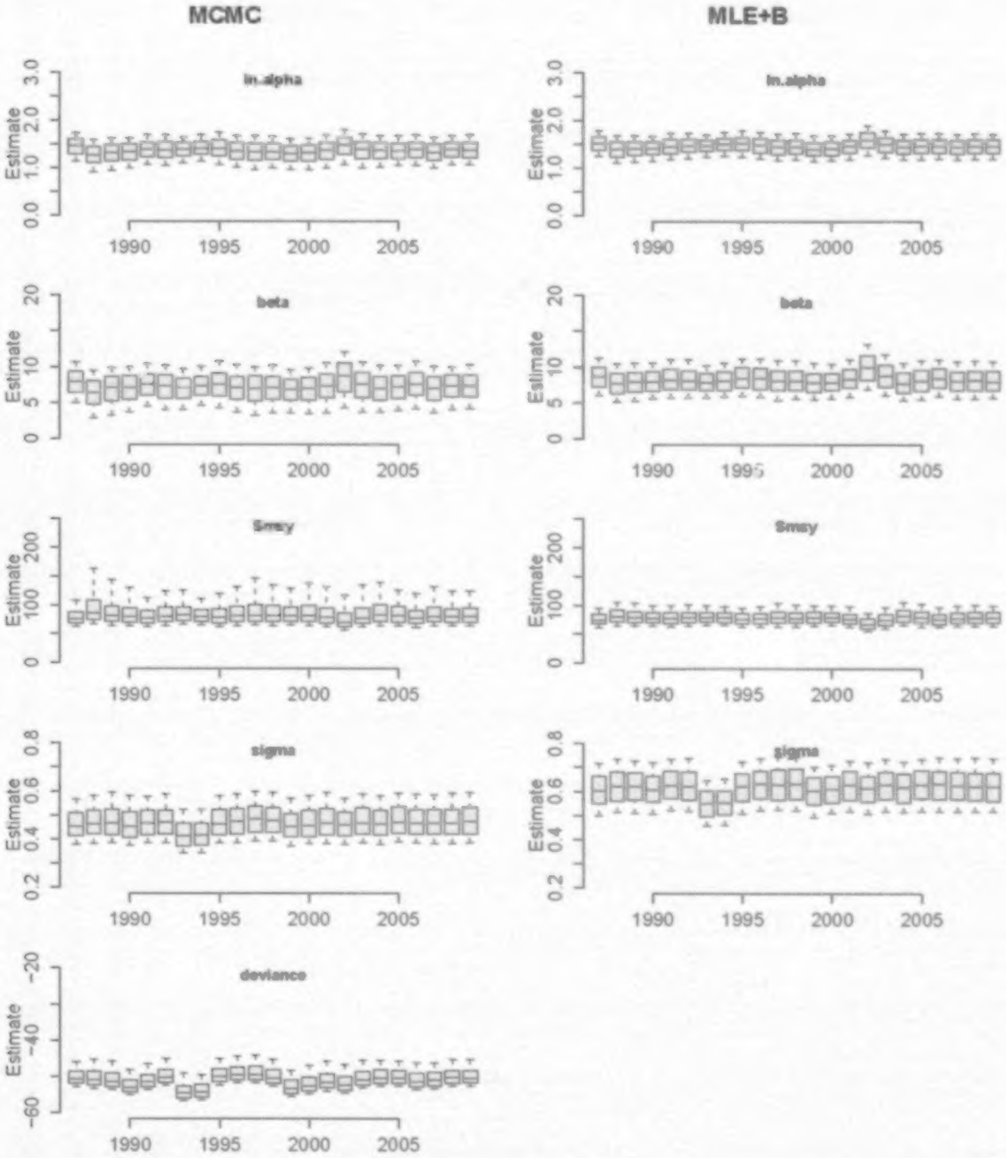


Figure 23: Jackknife Test of MLE+B vs MCMC - S_{MSY} for Ricker, Spn2Ad. All figures show the change in estimates as individual observations are dropped. Left panels show estimates for the basic Ricker fit using Bayesian MCMC with BRugs and OpenBUGS. Right panels show fits for the same data set and model form, just using simple linear regression and bootstrapping. The horizontal axes identify the brood year that was dropped from the data set.

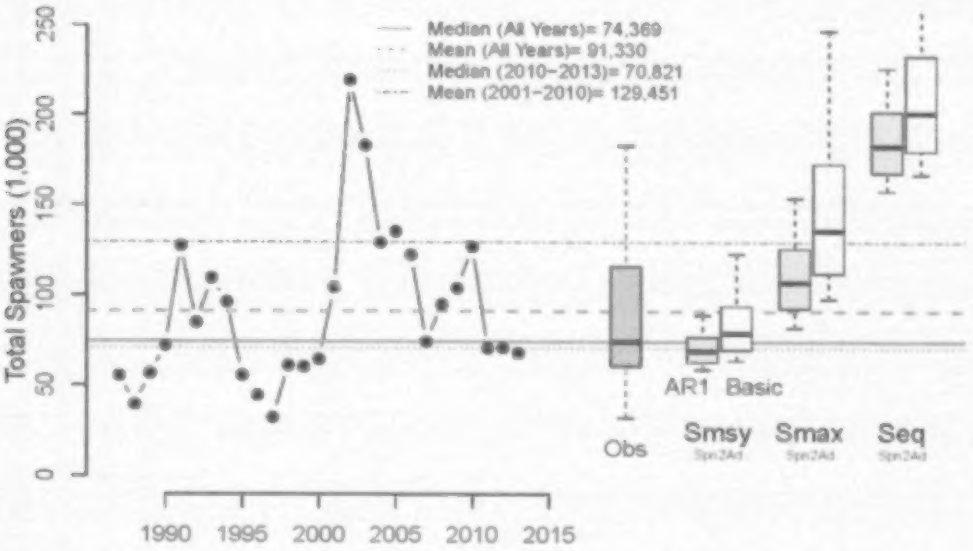


Figure 24: Observed Spn compared to biological benchmarks for 2 alternative forms of the Ricker model. Observed time series of spawners is the same data as plotted in Figure 1. Boxplots show the range of observed values and posterior distributions of benchmark estimates (p10, p25, median, p75, p90). Table 1 defines the benchmarks and Table 5 lists the equations used to calculate them. Figure 8 illustrates the benchmark definitions. The two Ricker model forms have the same general properties, but the Ricker AR1 form corrects for observed patterns in residuals (Table 4) and is the CSAS-recommended model form (Section 5.1.2).

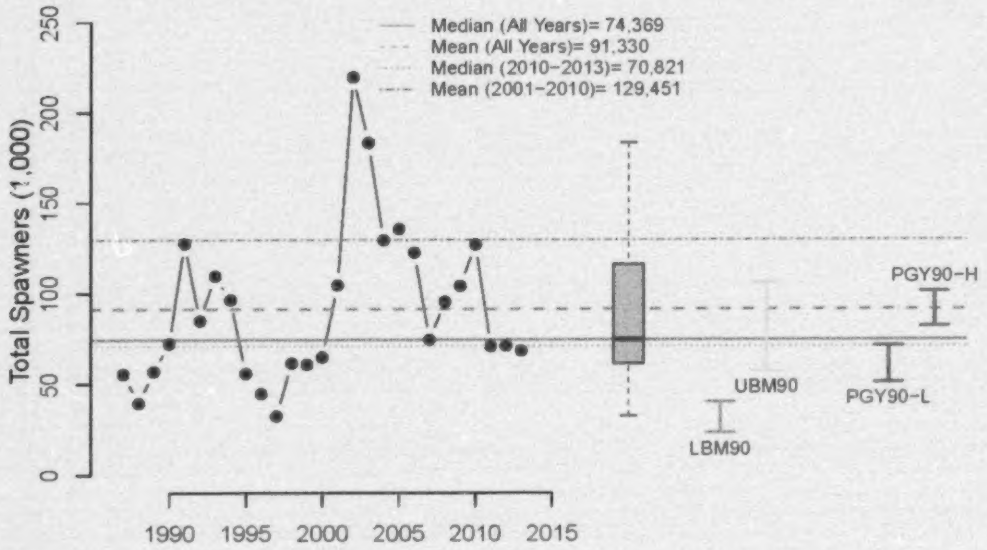


Figure 25: Observed Spn compared to proposed Summary Reference Points (SRP). Observed time series of spawners is the same data as plotted in Figure 1. The grey boxplot shows the range of observed values (p10, p25, median, p75, p90). Reference ranges show spread in Summary Reference Points (SRP) across 4 adult data sets and 3 alternative SR models (i.e. values from bottom of Table 13). LBM90 and UBM90 capture status considerations under Canada's Wild Salmon Policy, while PGY90 captures yield considerations. Section 2.5 defines the SRP.

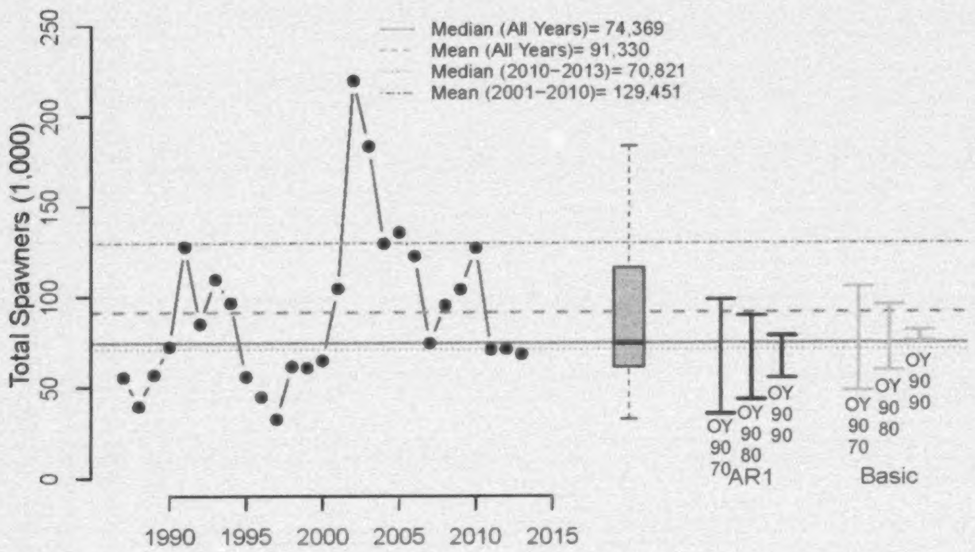


Figure 26: Observed Spn compared to ADFG-style reference ranges. Observed time series of spawners is the same data as plotted in Figure 1. The grey boxplot shows the range of observed values (p10, p25, median, p75, p90). Reference ranges show probability of achieving 70, 80, or 90% of MSY based on the ADFG-type calculation approach (i.e. the yield-based reference ranges in the right-most column of Table 16). The two Ricker model forms have the same general properties, but the Ricker AR1 form corrects for observed patterns in residuals (Table 4) and is the CSAS-recommended model form (Section 5.1.2).

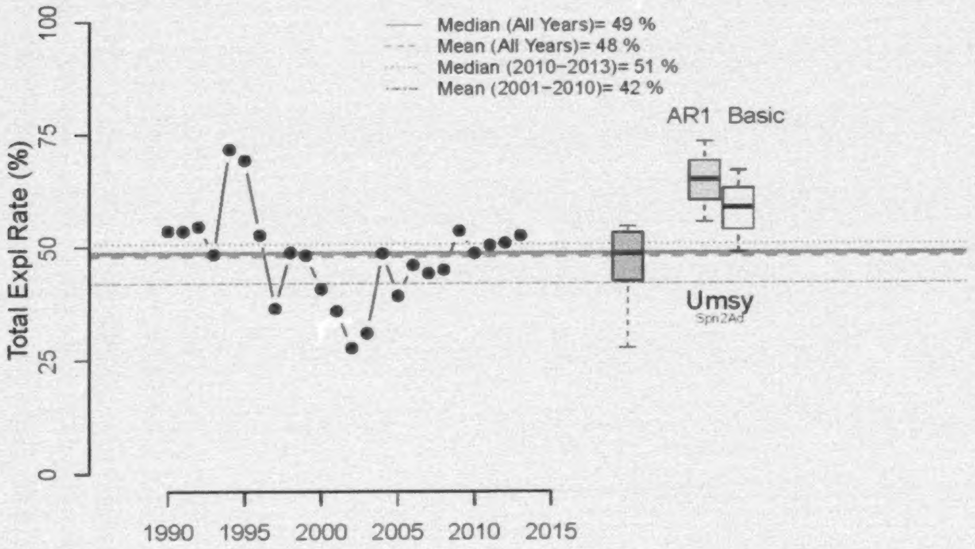


Figure 27: Observed ER compared to estimate of ER at MSY (U_{MSY}). Observed time series of ER is the same data as plotted in Figure 7. Annual estimates are listed in Appendix Table A 1. Boxplots show the range of observed values and posterior distributions of benchmark estimates (p10, p25, median, p75, p90). Table 1 defines the benchmark and Table 5 lists the equation used to calculate it. The two Ricker model forms have the same general properties, but the Ricker AR1 form corrects for observed patterns in residuals (Table 4) and is the CSAS-recommended model form (Section 5.1.2).

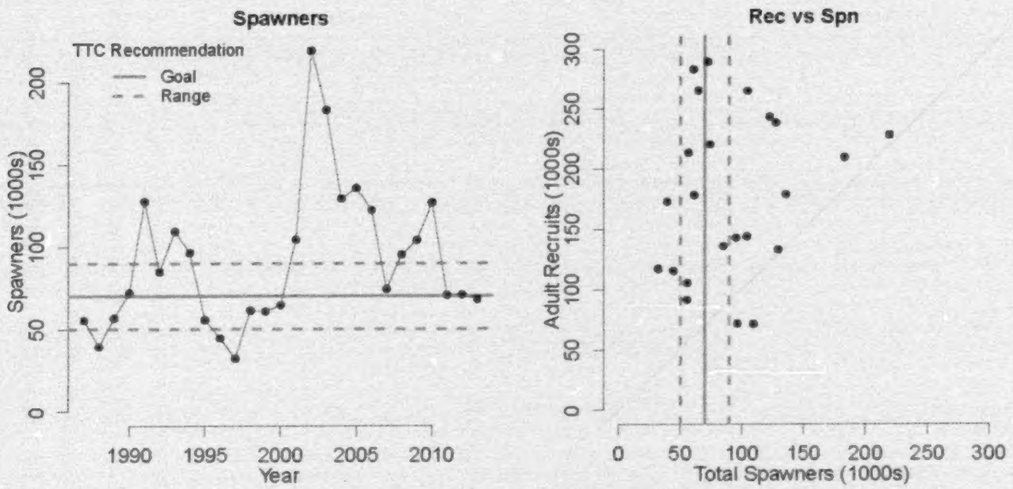


Figure 28: TTC-recommended Spawning Goal Range compared to SR data. The left panel shows TTC-recommended goal range of 70,000 ± 20,000 spawners relative to the observed time series of total spawners. 3 early observations have fallen below the lower end of the range (1988, 1996, 1997), but most of the 27 available observations have been within or above the goal range. The right panel shows goal range relative to the scatterplot of recruits vs. spawners, and highlights the wide range of observed recruit abundances for this comparatively narrow range of spawner abundances, with the range in recruitment about 6 times larger than the range in spawner abundance. Appendix Table A 1 shows that observed recruits varied from 91,319 to 289,431 fish for spawner abundances between 55,457 to 84,901 fish. Also note that the two lowest observed recruitments were from brood years with spawner abundances slightly above the goal range (i.e. 1993 and 1994 data points below the diagonal replacement line).

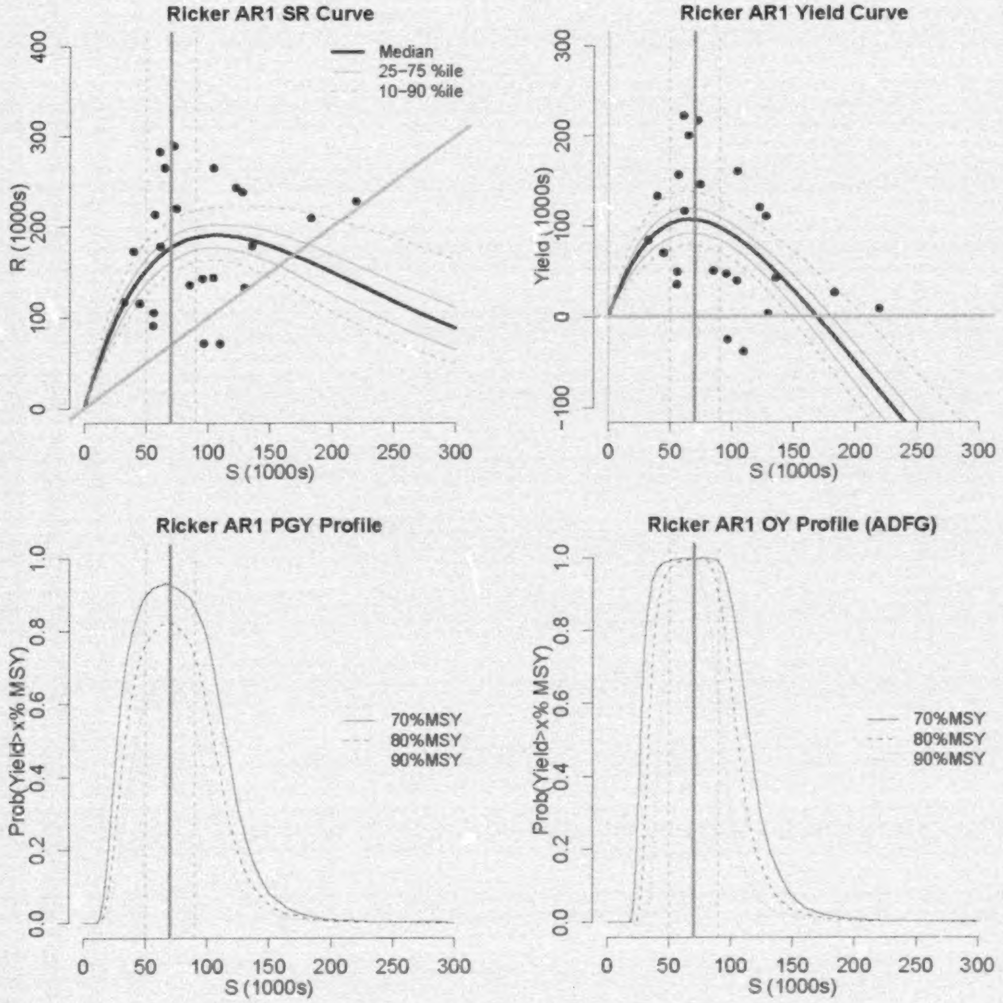


Figure 29: TTC-recommended Spawning Goal Range compared to SR model fits for the CSAS recommended model-data combination. This figure compares the TTC-recommended goal range of 70,000 ± 20,000 spawners to diagnostic plots for the CSAS-recommended model-data combination (see rationale in Section 5.1.2). The diagnostic plots are described in the original figures: SR curve in Figure 11, yield curve in Figure 12, and yield profiles in Figure 15.

10. APPENDIX A: DATA

Table A 1: Taku Coho Brood Table. Canyon Island = Canyon Island fishwheel data. Comm & Test = Data from Canadian commercial fishery and test fishery

Brood Year	**Total Spawners**	**% Females** Canyon Island	**Female Spawners**	**Smolts**	**Adult Recruits** Canyon Island	**Adult Recruits** Comm & Test	**Total Expl. Rate**
1987	55,457	38.8%	21,503	-	91,319	91,319	-
1988	39,450	43.0%	16,965	-	173,090	173,090	-
1989	56,808	40.0%	22,723	-	213,705	213,705	-
1990	72,196	39.2%	28,327	1,406,991	289,431	289,431	54%
1991	127,484	48.7%	62,061	850,295	238,606	238,606	54%
1992	84,901	35.6%	30,216	1,677,571	135,887	135,887	55%
1993	109,457	39.8%	43,558	1,206,137	71,302	71,302	48%
1994	96,343	38.9%	37,436	800,916	71,632	71,632	72%
1995	55,710	36.1%	20,097	910,234	105,445	126,904	69%
1996	44,635	37.2%	16,597	905,220	115,296	126,528	53%
1997	32,345	40.4%	13,055	1,219,478	117,212	131,072	36%
1998	61,382	36.8%	22,607	1,958,355	178,437	278,798	49%
1999	60,768	37.0%	22,481	2,163,672	283,156	256,294	48%
2000	64,699	45.7%	29,577	2,512,608	265,219	244,522	41%
2001	104,394	40.9%	42,688	2,875,673	265,032	222,452	36%
2002	219,360	33.2%	72,826	2,649,596	228,334	225,130	28%
2003	183,112	50.8%	92,940	3,586,753	209,731	209,488	31%
2004	129,327	47.6%	61,610	2,728,703	132,979	159,361	49%
2005	135,558	39.3%	53,287	2,597,875	178,851	149,721	39%
2006	122,384	43.4%	53,125	2,415,208	243,461	299,006	46%
2007	74,369	37.2%	27,675	2,388,118	220,629	144,058	44%
2008	95,226	41.9%	39,857	2,129,566	142,846	163,518	45%
2009	103,950	40.9%	42,536	1,514,210	143,944	140,631	54%
2010	126,830	41.2%	52,231	1,439,777	-	-	49%
2011	70,745	-	-	-	-	-	50%
2012	70,897	-	-	-	-	-	51%
2013	68,118	-	-	-	-	-	53%
Avg	**91,330**	**40.6%**	**38,582**	**1,901,760**	**178,937**	**180,976**	**48%**
Min	32,345	33.2%	13,055	800,916	71,302	71,302	28%
p15	55,685	36.9%	20,730	910,234	108,400	126,641	37%
p25	61,075	37.2%	22,576	1,219,478	125,095	133,480	43%
Median	**74,369**	**39.9%**	**33,826**	**1,958,355**	**178,437**	**163,518**	**49%**
p75	115,921	42.1%	52,455	2,512,608	233,470	231,868	53%
p85	127,668	44.7%	57,865	2,649,596	258,560	252,763	54%
Max	219,360	50.8%	92,940	3,586,753	289,431	299,006	72%

*Table A 2: Estimated Observation Errors for Total Spawners and Adult Recruits (Base-case Data Set). Section 2.1.1 describes how annual estimates and their standard error are derived. CV is the coefficient of variation, calculated as CV = (Std Dev / Mean) *100.*

Brood Year	**Total Spawners**			**Adult Recruits**		
	Mean	**St. Dev.**	**CV**	**Mean**	**St. Dev.**	**CV**
1987	55,457	4,053	**7**	91,319	6,363	**7**
1988	39,450	7,162	**18**	173,090	15,236	**9**
1989	56,808	11,174	**20**	213,705	22,537	**11**
1990	72,196	21,813	**30**	289,431	25,552	**9**
1991	127,484	11,174	**9**	238,606	19,570	**8**
1992	84,901	19,033	**22**	135,887	8,474	**6**
1993	109,457	17,503	**16**	71,302	5,064	**7**
1994	96,343	6,529	**7**	71,632	5,029	**7**
1995	55,710	3,242	**6**	105,445	7,153	**7**
1996	44,635	3,650	**8**	115,296	7,941	**7**
1997	32,345	4,120	**13**	117,212	6,279	**5**
1998	61,382	5,394	**9**	178,437	10,497	**6**
1999	60,768	7,049	**12**	283,156	25,317	**9**
2000	64,699	5,667	**9**	265,219	18,956	**7**
2001	104,394	9,495	**9**	265,032	18,135	**7**
2002	219,360	28,648	**13**	228,334	27,604	**12**
2003	183,112	17,724	**10**	209,731	10,543	**5**
2004	129,327	12,301	**10**	132,979	12,413	**9**
2005	135,558	30,685	**23**	178,851	16,898	**9**
2006	122,384	8,643	**7**	243,461	10,954	**4**
2007	74,369	13,608	**18**	220,629	12,164	**6**
2008	95,226	15,062	**16**	142,846	5,881	**4**
2009	103,950	7,025	**7**	143,944	5,371	**4**
2010	126,830	8,304	**7**	-	-	-
2011	70,745	4,730	**7**	-	-	-
2012	70,897	3,569	**5**	-	-	-
2013	68,118	3,214	**5**	-	-	-
Min	32,345	3,214	**5**	71,302	5,029	**4**
Median	**74,369**	**8,304**	**9**	**178,437**	**10,954**	**7**
Max	219,360	30,685	**30**	289,431	27,604	**12**

Table A 3: Taku Coho Catch by Harvest Sector. Data provided by ADFG and DFO staff. US harvests based on CWT expansion. Canadian recreational harvest believed to be negligible.

	US						Canadian					
Year	Troll	Gillnet	Seine	Rec	Pers. Use	Total US Catch	Comm. Gillnet	First Nation	Test fishery	Total Cdn Catch	Total Catch	% US Troll
1992	41,713	9,013	2,283	431	88	123,528	4077	187	1277	5,541	129,069	32.32%
1993	78,371	40,308	3,430	3,222	25	125,356	3033	8	1593	4,634	129,990	60.29%
1994	97,039	86,198	26,352	19,018	93	228,700	14531	162	-	14,693	243,393	39.87%
1995	45,041	56,820	1,853	7,857	97	111,668	13629	109	-	13,738	125,406	35.92%
1996	24,779	17,069	220	2,461	67	44,596	5028	24	-	5,052	49,648	49.91%
1997	8,822	1,489	621	4,963	27	15,922	2594	96	-	2,690	18,612	47.40%
1998	28,827	19,371	742	4,427	86	53,453	5090	0	-	5,090	58,543	49.24%
1999	36,231	7,507	2,881	4,170	44	50,833	4416	471	688	5,575	56,408	64.23%
2000	21,236	11,466	2,132	4,137	31	39,002	4395	342	710	5,447	44,449	47.78%
2001	38,326	11,777	2,065	3,094	22	55,284	2568	500	31	3,099	58,383	65.65%
2002	39,053	30,894	3,456	6,642	68	80,113	3082	688	32	3,802	83,915	46.54%
2003	36,433	27,694	3,646	10,503	59	78,335	3168	416	59	3,643	81,978	44.44%
2004	62,002	30,961	5,335	14,108	120	112,526	5966	450	3268	9,684	122,210	50.73%
2005	46,521	23,546	4,325	4,654	134	79,180	4924	162	3173	8,259	87,439	53.20%
2006	49,394	37,879	613	4,621	134	92,641	8567	300	2802	11,669	104,310	47.35%
2007	23,519	18,795	6,484	2,124	60	50,982	5244	155	2674	8,073	59,055	39.83%
2008	47,997	25,254	-	1,530	91	74,872	3906	67	0	3,973	78,845	60.88%
2009	51,748	46,838	4,749	6,720	240	110,295	5649	154	3963	9,766	120,061	43.10%
2010	34,554	52,497	3,988	14,287	258	105,584	10349	59	4000	14,408	119,992	28.80%
2011	23,825	11,353	6,383	4,804	224	46,589	8460	142	4002	12,604	59,193	40.25%
2012	14,648	12,108	-	1,212	121	28,088	11581	169	2200	13,950	42,038	34.84%
2013	34,849	24,986	2,372	2,472	189	64,869	10263	111	0	10,374	75,243	46.32%
Median	**37,380**	**24,266**	**3,156**	**4,524**	**90**	**76,604**	**5,059**	**159**	**1,593**	**6,824**	**80,412**	**46.95%**

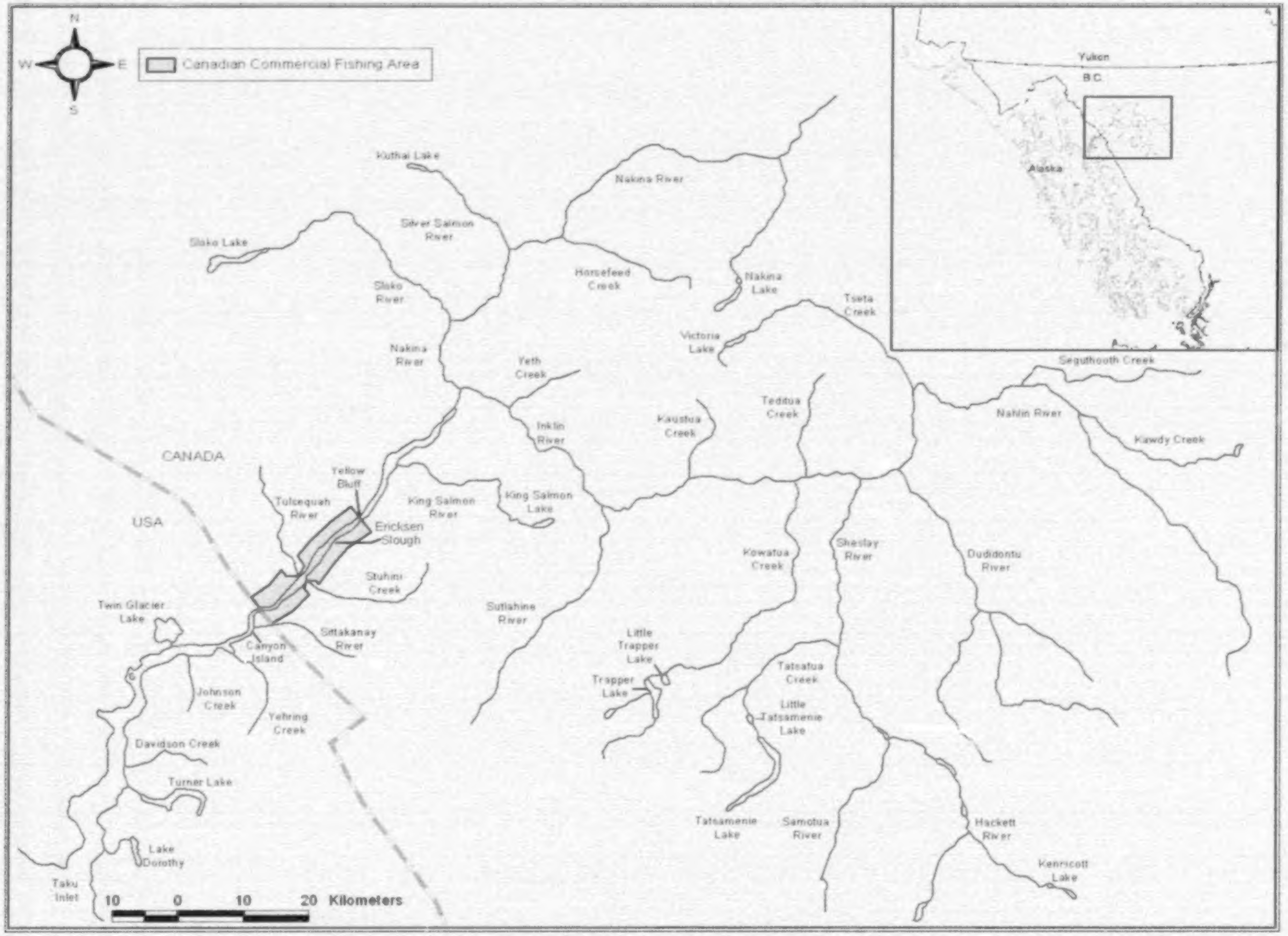

N
W
E
S
Canadian Commercial Fishing Area
Yukon
B.C.
Alaska
Kuthai Lake
Nakina River
Silver Salmon River
Sloko Lake
Horsefeed Creek
Nakina Lake
Sloko River
Tseta Creek
Victoria Lake
Nakina River
Yeth Creek
Seguthooth Creek
Teditua Creek
Kaustua Creek
Nahlin River
Inklin River
Kawdy Creek
CANADA
Yellow Bluff
Tulsequah River
King Salmon River
King Salmon Lake
USA
Ericksen Slough
Kowatua Creek
Shesley River
Dudidontu River
Stuhini Creek
Sutlahine River
Twin Glacier Lake
Sittakanay River
Canyon Island
Little Trapper Lake
Tatsatua Creek
Trapper Lake
Johnson Creek
Little Tatsamenie Lake
Yehring Creek
Davidson Creek
Turner Lake
Tatsamenie Lake
Samotua River
Hackett River
Lake Dorothy
Kenricott Lake
Taku Inlet
10
0
10
20
Kilometers

Figure A 1: Map of Taku River Watershed. Map taken from 2014 Integrated Fisheries Management Plan (DFO 2014)

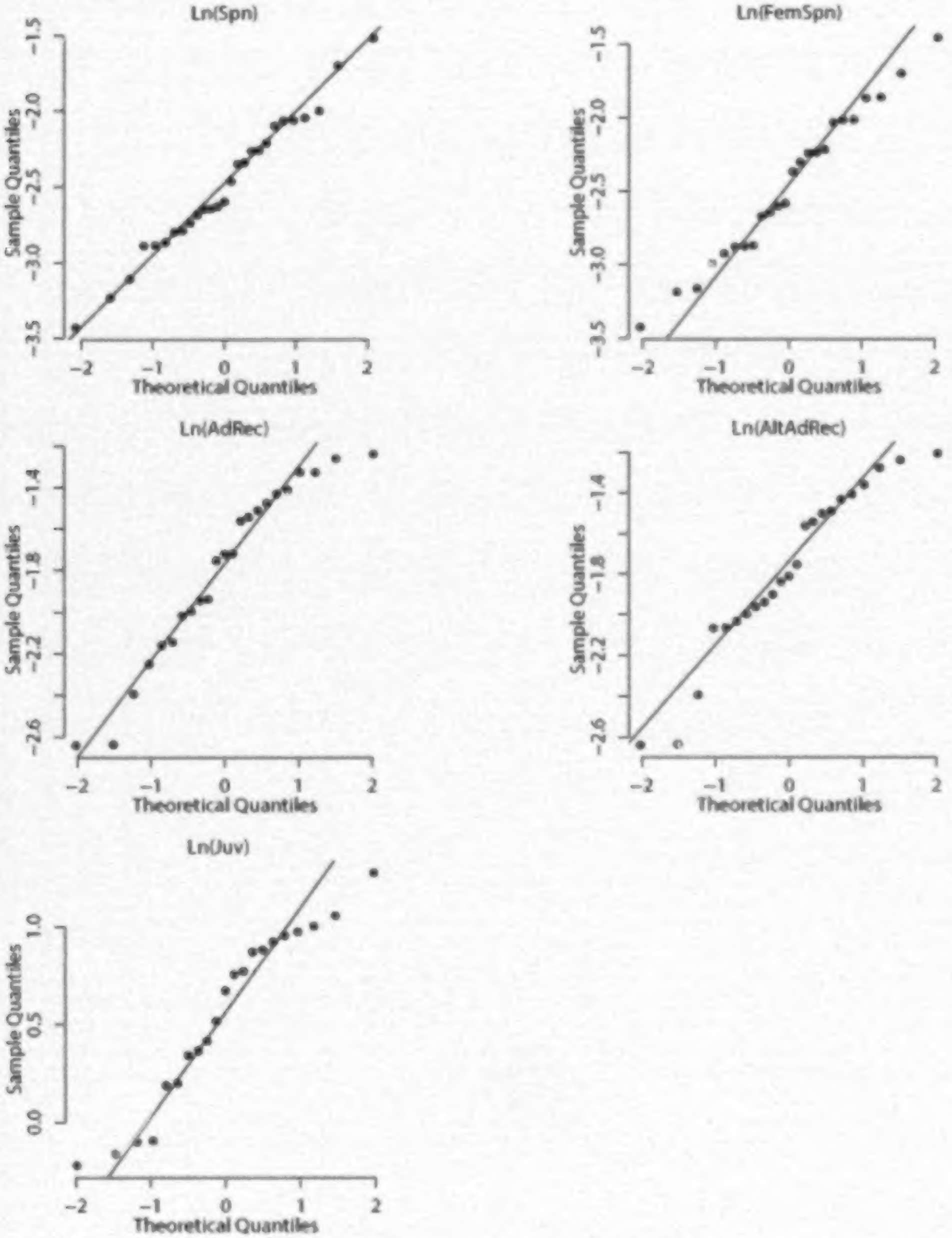


Figure A 2: QQnorm plots of Taku Coho Data. Each panel compares the percentiles of a log-transformed data set to a theoretical normal distribution. If data is log-normally distributed, the log() of the estimates should resemble a normal distribution. If the distributions match, the points fall close to the diagonal line.

11. APPENDIX B: BUGS/JAGS MODEL FILES

11.1. SAMPLE DATA AND INITS FILES

```
# inits.txt file used for BRugs()
# initiates two sample chains for the MCMC

list(tau_R=3)
list(tau_R=7)




# data.txt file used for BRugs() - Spn2AD data set

list(N= 23 ,
S=c(
0.055457,0.039450,0.056808,0.072196,0.127484,0.084901,0.109457,0.096343,0.055710,0.044635,0.032345,0.061382
,0.060768,0.064699,0.104394,0.219360,0.183112,0.129327,0.135558,0.122384,0.074369,0.095226,0.103950
) ,
R_Obs=c(
0.091319,0.173090,0.213705,0.289431,0.238606,0.135887,0.071302,0.071632,0.105445,0.115296,0.117212,0.178437
,0.283156,0.265219,0.265032,0.228334,0.209731,0.132979,0.178851,0.243461,0.220629,0.142846,0.143944
)
)
```

11.2. RICKER MODEL

```
# Ricker model
# taken from code package by Cass, Huang, Porszt, Grant, Macdonald, Michielsens
# parts that are not SR par estimation were moved to R to speed up the overall performance
# Notation translator:  Y[] = "Ln(R.pred)" ,  RS[] = "Ln(RperS)", alpha ="ln.alpha"


model{
    for (i in 1:N) {                        #loop over N sample points
    R_Obs[i] ~ dlnorm(Y[i],tau_R)           #likelihood
    Y[i] <- RS[i] +log(S[i])                #calc log(R)
    RS[i] <- alpha - beta * S[i]           # ricker model
    log.resid[i] <-  log(R_Obs[i]) - Y[i]  # tracking residuals for diagnostics
   }


    alpha ~ dnorm(0,0.0001)               #prior for alpha
    beta <-1/C                               # prior for beta
    C~ dlnorm(1,0.1)                         # prior for beta

    tau_R ~ dgamma(0.001,0.001)                     #prior for precision parameter

    sigma <- 1/sqrt(tau_R)                      # changed to this based on
                                                # Fleischman and Evenson (2010) ADFG FMS10-04

}
```

11.3. RICKER AR1 MODEL

```
# Ricker model with 1-yr autoregression term
# Adapted from code package by Cass, Huang, Porszt, Grant, Macdonald, Michielsens
# and expanded for AR1 based on Eq21 and 22 of Fleischman and Evenson (2010) ADFG FMS10-04
# parts that are not SR par estimation are handled in R to speed up the overall performance
# Notation translator:  Y[] = "Ln(R.pred)" ,  RS[] = "Ln(RperS)", alpha ="ln.alpha"

model{

   # do first year
   R_Obs[1] ~ dlnorm(Y[1],tau_R)
   Y[1] <- log(S[1]) + RS[1]
   RS[1] <- alpha - beta * S[1] + phi * log.resid.0

   # do second year
   R_Obs[2] ~ dlnorm(Y[2],tau_R)
   Y[2] <- log(S[2]) + RS[2]
   RS[2] <- alpha - beta * S[2] + phi * log.resid[1]
   log.resid[1] <-  log(R_Obs[1]) - Y[1]

   #loop over ret of N sample points (starting with the third)
   for (i in 2:N) { log.resid[i] <-  log(R_Obs[i]) - Y[i] }
   for (i in 3:N) {
                        R_Obs[i] ~ dlnorm(Y[i],tau_R)  # likelihood
                        Y[i] <- log(S[i]) + RS[i]
                            RS[i] <- alpha - beta * S[i] + phi * log.resid[i-1]
                  } # end for loop

    alpha ~ dnorm(0,0.0001)            #prior for alpha
    beta <-1/C                         # prior for beta
    C ~ dlnorm(1,0.1)                  # prior for beta -> could change to dlnorm(p.beta, tau_beta)
    tau_R ~ dgamma(0.001,0.001)           #prior for precision parameter
    phi ~ dnorm(0,0.0001)I(-1,1)          # AR1 priors as per Fleishman and Evenson AppA2
    log.resid.0 ~ dnorm(0,tau.red)  # I(-3,3)  remove for jags  WHY?
    tau.red <- tau.white * (1-phi*phi)
    tau.white ~ dgamma(0.01,0.01)
    sigma <- 1/sqrt(tau_R)                      # based on Fleishman and Evenson (2010) ADFG FMS10-04
} # end model description
```

11.4. RICKER KALMAN FILTER MODEL

```
# Ricker with Kalman filter model
# Modified from code by Catherine Michielsens
# Changes include:
#  - moved all calculations that are not SR par estimation to R for speeding up performance
#  - slightly modified notation for consistency with other model code used in this project (ln.alpha vs.
      alpha, etc)

model{
for (i in 1:N){
   R_Obs[i] ~ dlnorm(Y[i],tau_R)           #likelihood
   Y[i] <- RS[i] +log(S[i])                #calc log(R)
   RS[i] <- ln.alpha[i] - beta * S[i] + v[i]
   v[i] ~dnorm(0, tauv)
    year[i]<-i
    Rep[i] ~ dlnorm(Y[i],tau_R)
    log.resid[i] <-  log(R_Obs[i]) - Y[i]  # tracking residuals for diagnostics
}
for (i in 2:N){
   ln.alpha[i] <- ln.alpha[i-1] + w[i]
   w[i]~ dnorm(0,tauw)
}
ln.alpha[1]~ dnorm(p.alpha,tau_alpha)
beta ~ dlnorm(1,0.1)
p.dummy<- p.beta
tau_dummy<-tau_beta
tau_R~ dgamma(0.01,0.001)
tauv ~ dgamma(0.01,0.001)
tauw~ dgamma(0.01,0.001)

sigma <- 1/sqrt(tau_R)                          # based on Fleishman and Evenson(2010) ADFG FMS10-04

}
```

12. APPENDIX C: R CODE

12.1. PERCENT RANK

The typical approach for displaying patterns that differ by several orders of magnitude (e.g. hundreds to millions of fish) is to plot the time series on a log scale. However this creates problems for visual interpretation, particularly with the diverse audiences in collaborative planning processes. The plots based on percent ranks are an experimental alternative.

Percent ranks rescale the smallest observation as 0, the largest observation as 1, and the median as 0.5. This puts all time series on the same vertical axis and gives the values a more direct interpretation.

Code adapted from FigRs.

```
# FUNCTION TO IMITATE EXCEL’S PERCENTRANK() FUNCTION
perc.rank<-function(x){
      rank.x<-rank(x, ties.method="min",na.last="keep")  # keep NAs as NA value
      perc.rank.x <- (rank.x-1)/(max(rank.x,na.rm=TRUE)-1)
      perc.rank.x
      }


# FUNCTION TO PLOT PERCENTRANKS AS DEVIATIONS FROM MEDIAN
perc.rank.plot<-function(x,ma=NULL,yrs=1990:2010,type="fancy"){
# x is a time series stored in vector
# ma specifies whether to plot a moving average. if ma is a number it defines the period

if(type=="spark"){barplot(perc.rank(x)-0.5, ylim=c(-0.5,0.5),col="darkblue",border="darkblue",
xlab="", ylab="",axes=FALSE,axisnames=FALSE)}

if(type=="fancy"){
x.ticks<-barplot(perc.rank(x)-0.5, ylim=c(0.6,0.5),col="lightblue",border="lightblue",
xlab="", ylab="",axes=FALSE,axisnames=FALSE)
abline(h=c(-0.5,0,0.5),col="gray")
      text(rep(-1.3,3), c(-0.5,0,0.5),adj=1,labels=c("Min","Median","Max"),xpd=NA,cex=0.9)
      if(!is.null(ma)){lines(x.ticks,filter(perc.rank(x)-
0.5,filter=rep(1/ma,ma),sides=1),col="red",lwd=2)}
      axis(side=1,at=x.ticks[seq(4,25,by=5)],labels= yrs[seq(4,25,by=5)])
      } # end type=fancy
}
```

12.2. PERCENTILE METHOD

```
# FUNCTION TO APPLY PERCENTILE METHOD AS DESCRIBED IN VOLK ET AL 2009 FMS 09-07

Percentile.Method <- function(spn,method="ADFG",rounding = TRUE, out.label="Data"){

# spn is a matrix with rows = years and 1 col labelled with the name of the dataset
# method either "ADFG" with %ile range changing depending on contrast in data or DFO which is always 25/75
# NOTE: output also includes all the %iles used in either method
# if rounding is turned on, then round UP to 2 sig fig as in Volk et al 2009

perc.vec <- seq(0.05,0.95,by=0.05)
if(rounding){ spn <- sapply(spn,FUN=roundup) }
contrast <- max(spn,na.rm=TRUE)/min(spn,na.rm=TRUE)
      if(method=="DFO"){perc.vals <- c(0.25,0.75);perc.labels <- c("SEG_L","SEG_H")}
      if(method=="ADFG"){
            if(contrast<4){perc.vals <- c(NA,0.15,1);perc.labels <- c("SEG_L_LowER","SEG_L","SEG_H")}
            if(contrast>=4 & contrast<=8 ){perc.vals <- c(NA,0.15,0.85);perc.labels <- c("SEG_L_LowER",
                                                                                           "SEG_L","SEG_H")}
            if(contrast>8){perc.vals <- c(0.15,0.25,0.75);perc.labels <- c("SEG_L_LowER","SEG_L","SEG_H")}
            } # end if method== "ADFG"

matrix.labels <- c("contrast",perc.labels,"min",paste("p",perc.vec*100,sep=""),"max")
out.matrix<- matrix(NA,nrow=length(matrix.labels),ncol=1,dimnames=list(c(matrix.labels), out.label))
out.matrix["contrast",] <- contrast
out.matrix[c("min","max"),]  <- c(min(spn,na.rm=TRUE),max(spn,na.rm=TRUE))
out.matrix[perc.labels,] <- quantile(spn,probs=perc.vals,na.rm=TRUE)
out.matrix[paste("p",perc.vec*100,sep=""),] <-  quantile(spn,probs=perc.vec,na.rm=TRUE)
out.matrix
} # end Percentile.Method

# ROUNDING SUB FUNCTION AS DESCRIBED IN VOLK ET AL 2009 FMS 09-07

roundup <- function(x){
      x.out <- signif(x,digits=2) # round to 2 significant figures
      if(x.out<x) { # if it was rounded down, then add 1 to the second sig fig
            x.out <- x.out + as.numeric(paste(1,paste(rep(0,trunc(log10(x)-1)),collapse=""),sep="")) }
      x.out}
```

12.3. SMOLT-CAPACITY METHOD

```
# FUNCTION TO APPLY SMOLT_CAPACITY METHOD AS IN SHAUL & TYDINGCO 2006 FMS06-11

SmoltCap.Method <- function(data.obj=NULL,include=0.5,prod.vals=c(25.4,42.4,50.8)){

# data.obj is a matrix with rows = years and 2 col Spn and Smolt by BY
# include = number up to 1 specifying the proportion of data to include in the calculation
#                  i.e 0.25 means only the largest quarter of the spawner data
# prod.vals = 3 values for low, MSY, high level of productivity in terms of Smolt/Spawner at Smsy
#                  default values are taken from Table 3 of Shaul & Tydingco 2006

data.obj <- na.omit(data.obj); attributes(data.obj)$na.action <- NULL # drop any row with NA

# extract subset to be used
cut.off <- quantile(data.obj[,"Spn"],probs=include)
data.used <- data.obj[data.obj[,"Spn"]>=cut.off,]

range.est <- matrix(NA,
nrow=dim(data.used)[1],ncol=3,dimnames=list(dimnames(data.used)[[1]],c("Lower","MSY","Upper")))

range.est[,"Lower"] <- data.used[,"Smolt"] / prod.vals[3]
range.est[,"MSY"] <- data.used[,"Smolt"] / prod.vals[2]
range.est[,"Upper"] <- data.used[,"Smolt"] / prod.vals[1]

# avg smolts and then apply range
range.avg <- matrix(mean(data.used[,"Smolt"])/rev(prod.vals), nrow=1,dimnames=list("Avg",
                                                                  c("Lower","MSY","Upper")))
out.list <- list(input=data.obj,cut.off=cut.off,data.used=data.used,
                                    range.est=range.est,range.avg=range.avg)

out.list

} # end SmoltCap.Method
```

12.4. REGRESSION (MLE) FIT OF BASIC RICKER MODEL

```
# FUNCTION TO FIT LINEAR FORM OF BASIC RICKER MODEL

ricker.fit <- function(Rec,Spn,sigma.type="default",var.labels=c("Log(R/S)","Spawners"),bm=TRUE,
                    rec.units="Rec",bm.alpha.correct=FALSE){

# Rec = recruits time series // # Spn = spawner time series (any variation: EFS, ETS, TS, Smolts)
# sigma.type =  specifies the calculation to be used for sigma. "default" = R default residual sq error
# bm = if TRUE, calculate various population benchmarks
# bm.alpha.correct= if TRUE, use ln(alpha) +(sigma^2/2) instead of ln(alpha)
# rec.units = "Rec" is default, but can also feed in "lnRpS"
# Note: BM code replicates the calculations in a spreadsheet provided by Ed Jones (ADFG)

if(rec.units=="Rec"){lnRpS <- log(Rec/Spn)}  # convert to log recruits per spawner
if(rec.units=="lnRpS"){lnRpS <- Rec }        # if function input is already in units of ln(Rec/Spn)

fit <- lm(lnRpS~Spn)   # fit simple linear regression model
ln.alpha.par <- fit$coefficients[1]  # extract intercept
beta.par <- -fit$coefficients[2]      # extract slope
if(sigma.type=="default"){sigma.par <- summary(fit)$sigma} # OTHER VARIATIONS TO BE IMPLEMENTED

if(bm){      Smax.bm <- 1/beta.par
      if(bm.alpha.correct){
            Seq.bm <- (ln.alpha.par + sigma.par^2/2) / beta.par
            Smsy.bm <- (ln.alpha.par + sigma.par^2/2) / beta.par *(0.5-0.07*(ln.alpha.par + sigma.par^2/2))
            }
      if(!bm.alpha.correct){
            Seq.bm <- ln.alpha.par / beta.par
            Smsy.bm <- ln.alpha.par / beta.par *(0.5-0.07*ln.alpha.par)
            }
            Umsy.bm <- Smsy.bm * beta.par
} # end if bm
out.pars <- c(exp(ln.alpha.par),beta.par,sigma.par); names(out.pars) <- c("alpha","beta","sigma")
out.bm<- c(Smax.bm,Seq.bm,Smsy.bm,Umsy.bm); names(out.bm) <- c("Smax","Seq","Smsy","Umsy")
out.list <- list(Model="Ricker", Pars=out.pars, BM=out.bm, sigma.type=sigma.type, var.labels=var.labels,
residuals=fit$residuals) # NOTE: the residuals are in lnRpS not R
out.list
} # end function ricker.fit
```

12.5. BRUGS MCMC

This appendix lists the main BRugs commands used for MCMC. The full program code is set up to handle multiple data sets and process the output, and is therefore too long for this appendix. This code sequence adapted from code developed by Cass, Huang, Porszt, Grant, Macdonald, Michielsens.

```
require(BRugs); require(coda)                   # check/load required packages
modelCheck(“Name of Model File”)                 # check the model file
modelData(“Name of Data File”)                  # Read in the data file
modelCompile(numChains=settings$chains)   # Compile the model
modelInits(rep("inits.txt", 2))                  # load initial chain values
modelGenInits()                           # generate remaining initial values

# do the burn in (Note: default set to 0, so that you can see initial conditions in the diagnostic plots.
# If burn.in = 0, remember to discard early sampled by using beg argument in subsequent steps!
modelUpdate(settings$burn.in)

samplesSet(“list of nodes”)   # start storing the sample from the MCMC chain (a.k.a monitor the nodes)
                              # list of nodes differs by model type
modelUpdate(settings$beg)     # Do first set of  MCMC samples (1:beg) before tracking DIC,
                              # because dicStats doesn't allow discarding first beg samples
dicSet()                      # start tracking the DIC values
modelUpdate(settings$n-settings$beg) # Do rest of  MCMC samples (beg:n)

# Get BRugs package outputs with
samplesCoda(node,stem= ,beg= ,thin= ) # MCMC samples
samplesStats("*",beg=settings$beg)  # summaries for all tracked nodes
samplesHistory("*",beg= ,plot=FALSE,thin= ) #MCMC samples by chain
samplesDensity(node,beg=  , plot=TRUE,main=node) # posterior distribution for a node
samplesBgr("*",plot=TRUE)  # check convergence using BGR criterion
acf(“MCMC Samples”, plot=TRUE) # check autocorrelation
dicStats() # check statistical fit based on DIC

# Get coda package outputs with
coda.list <-  buildMCMC("*",beg=settings$beg,thin=settings$thin.codaplots)
xyplot(coda.list,ask=FALSE) ; densityplot(coda.list,ask=FALSE)
gelman.plot(coda.list,ask=FALSE) ; crosscorr.plot(coda.list,ask=FALSE)
cumuplot(coda.list,ask=FALSE) ; densplot(coda.list,ask=FALSE)
# default geweke plot crashes for some stocks  because needs finite ylim, can't set ylim=()
```

```
geweke.plot.MOD(coda.list,ask=FALSE)
```

12.6. R2JAGS MCMC

This appendix lists the main r2JAGS commands used for MCMC. The full program code is set up to handle multiple data sets and process the output, and is therefore too long for this appendix.

```
library(rjags); library(R2jags); library(coda) # check/load required packages

data.set <- na.omit(data object)

# Set up inputs (NOTE: var names must match JAGS model file exactly)
S <- data.set[,"Spn"]
R_Obs <-  data.set[,"Rec"]
N <- length(S)

jags.data <- list("S","R_Obs","N")


jagsfit <- jags(data=jags.data, inits=NULL,parameters.to.save=nodes, n.iter=settings$n,
            n.chains=settings$chains,n.burnin=settings$burn.in, model.file=”Name of Model File”)

# Get JAGS output, already thinned based on JAGS default
print("Output Elements"); print(names(jagsfit))
print("Model Fit"); print(jagsfit$model)
print("r2jags BUGS Output Elements"); print(names(jagsfit$BUGSoutput))
print("MCMC SubSample");print(jagsfit$BUGSoutput$sims.array[1:20,,])
jagsfit$BUGSoutput$sims.matrix
jagsfit$BUGSoutput$summary
jagsfit$BUGSoutput$DIC
plot(jagsfit) # basic plot
traceplot(jagsfit,ask=FALSE) # traceplot

# Get coda package outputs with
jagsfit.mcmc <- as.mcmc(jagsfit) # use diagnostics from coda package
#xyplot(jagsfit.mcmc)  # -> not creating any plots?
#densityplot(jagsfit.mcmc) # -> not creating any plots?
gelman.plot(jagsfit.mcmc)
crosscorr.plot(jagsfit.mcmc,main="crosscorr.plot")
cumuplot(jagsfit.mcmc)
densplot(jagsfit.mcmc)
```

```
geweke.plot(jagsfit.mcmc)
```

12.7. MEASURES OF FIT AND PRECISION

```
npcv.fn <- function(x) {
                x <- na.omit(as.vector(x))
                attributes(x)$na.action <- NULL
                quants <- quantile(x,probs=c(0.6915,0.3885,0.5))
                npcv <- (quants[1] - quants[2]) / quants[3]
                if(sign(min(x))<>sign(max(x))){npcv<-NA} # NPCV only works if sample range doesn't span 0
                npcv
                }

siqr.fn <- function(x) {
                x <- na.omit(as.vector(x))
                attributes(x)$na.action <- NULL
                quants <- quantile(x,probs=c(0.75,0.25,0.5))
                siqr <- (quants[1] - quants[2]) / quants[3]
                if(sign(min(x))<>sign(max(x))){siqr<-NA} # SIQR only works if sample range doesn't span 0
                siqr
                }

smad.fn <- function(x) {
                x <- na.omit(as.vector(x))
                attributes(x)$na.action <- NULL
                smad <- median(abs(x - median(x)))/median(x)
                smad
                }
```

13. APPENDIX D: POSTERIOR DISTRIBUTIONS OF MODEL PARAMETERS

Models, parameters, and datasets as described in Section 2.3.1. The CSAS- recommended model-data combination is shaded in the tables. The first set of figures in this section has the same layout as Figure 17, and shows results for the remaining model-data combinations. The last two figures show boxplots corresponding to the tables, as well as the resulting biological benchmark estimates.

Table D 1: Percentiles of posterior distributions for productivity parameters (alpha)

DataSet	Model	Parameter	p10	p25	p50	p75	p90
TC_Spn2Ad	Ricker	alpha	2.831	3.340	3.956	4.578	5.304
TC_Spn2AdAlt	Ricker	alpha	3.037	3.564	4.191	4.902	5.571
TC_Spn2Juv	Ricker	alpha	18.673	21.164	26.275	31.645	37.353
TC_FemSpn2Ad	Ricker	alpha	3.057	3.476	4.004	4.593	5.209
TC_FemSpn2AdAlt	Ricker	alpha	3.090	3.565	4.145	4.814	5.402
TC_FemSpn2Juv	Ricker	alpha	19.365	22.709	27.794	33.235	38.009
TC_Spn2Ad	**RickerAR1**	**alpha**	**3.550**	**4.162**	**4.858**	**5.692**	**6.547**
TC_Spn2AdAlt	RickerAR1	alpha	2.798	3.328	3.999	4.754	5.570
TC_Spn2Juv	RickerAR1	alpha	24.609	31.391	39.203	48.259	57.549
TC_FemSpn2Ad	RickerAR1	alpha	3.090	3.616	4.237	4.903	5.603
TC_FemSpn2AdAlt	RickerAR1	alpha	3.012	3.466	4.067	4.716	5.400
TC_FemSpn2Juv	RickerAR1	alpha	26.617	32.317	39.127	46.911	55.319
TC_Spn2Ad	RickerK	alpha*	2.143	2.683	3.165	3.896	4.758
TC_Spn2AdAlt	RickerK	alpha*	1.819	2.420	3.143	4.004	4.993
TC_Spn2Juv	RickerK	alpha*	26.899	32.053	38.567	45.853	54.555
TC_FemSpn2Ad	RickerK	alpha*	2.578	2.892	3.446	4.107	4.717
TC_FemSpn2AdAlt	RickerK	alpha*	2.021	2.427	3.070	3.695	4.410

* 2009 Brood Year

Table D 2: Percentiles of posterior distributions for capacity parameters (beta)

DataSet	Model	Parameter	p10	p25	p50	p75	p90
TC_Spn2Ad	Ricker	beta	4.055	5.839	7.375	8.946	10.325
TC_Spn2AdAlt	Ricker	beta	4.755	6.322	7.832	9.346	10.776
TC_Spn2Juv	Ricker	beta	0.053	0.667	3.030	5.326	6.763
TC_FemSpn2Ad	Ricker	beta	4.809	6.092	7.409	8.723	9.907
TC_FemSpn2AdAlt	Ricker	beta	4.825	6.271	7.627	9.036	10.166
TC_FemSpn2Juv	Ricker	beta	0.185	1.733	3.694	5.342	6.711
TC_Spn2Ad	**RickerAR1**	**beta**	**6.473**	**7.961**	**9.351**	**10.806**	**12.140**
TC_Spn2AdAlt	RickerAR1	beta	3.768	5.424	7.272	8.958	10.363
TC_Spn2Juv	RickerAR1	beta	3.067	5.275	7.429	9.357	10.883
TC_FemSpn2Ad	RickerAR1	beta	5.337	6.688	8.037	9.357	10.536
TC_FemSpn2AdAlt	RickerAR1	beta	4.656	6.149	7.431	8.699	9.828
TC_FemSpn2Juv	RickerAR1	beta	3.576	5.331	7.136	8.625	10.101
TC_Spn2Ad	RickerK	beta	4.099	6.360	7.872	9.361	10.634
TC_Spn2AdAlt	RickerK	beta	2.118	5.593	7.597	9.421	11.031
TC_Spn2Juv	RickerK	beta	6.435	7.783	9.238	10.517	11.705
TC_FemSpn2Ad	RickerK	beta	6.365	7.274	8.511	9.992	11.173
TC_FemSpn2AdAlt	RickerK	beta	4.044	5.439	7.374	8.938	10.255
TC_FemSpn2Juv	RickerK	beta	6.253	7.563	8.885	10.217	11.763

Table D 3: Percentiles of posterior distributions for error parameters (sigma)

DataSet	Model	Parameter	p10	p25	p50	p75	p90
TC_Spn2Ad	Ricker	sigma	0.383	0.417	0.462	0.513	0.570
TC_Spn2AdAlt	Ricker	sigma	0.379	0.413	0.458	0.511	0.569
TC_Spn2Juv	Ricker	sigma	0.373	0.409	0.450	0.509	0.568
TC_FemSpn2Ad	Ricker	sigma	0.377	0.409	0.453	0.505	0.561
TC_FemSpn2AdAlt	Ricker	sigma	0.376	0.410	0.454	0.505	0.565
TC_FemSpn2Juv	Ricker	sigma	0.366	0.404	0.450	0.511	0.572
TC_Spn2Ad	**RickerAR1**	**sigma**	**0.266**	**0.291**	**0.324**	**0.363**	**0.409**
TC_Spn2AdAlt	RickerAR1	sigma	0.307	0.337	0.376	0.425	0.474
TC_Spn2Juv	RickerAR1	sigma	0.285	0.313	0.356	0.405	0.456
TC_FemSpn2Ad	RickerAR1	sigma	0.304	0.331	0.367	0.413	0.465
TC_FemSpn2AdAlt	RickerAR1	sigma	0.295	0.322	0.358	0.403	0.454
TC_FemSpn2Juv	RickerAR1	sigma	0.313	0.341	0.383	0.434	0.490
TC_Spn2Ad	RickerK	sigma	0.035	0.056	0.092	0.152	0.221
TC_Spn2AdAlt	RickerK	sigma	0.045	0.073	0.127	0.201	0.297
TC_Spn2Juv	RickerK	sigma	0.039	0.059	0.100	0.155	0.202
TC_FemSpn2Ad	RickerK	sigma	0.029	0.042	0.073	0.127	0.193
TC_FemSpn2AdAlt	RickerK	sigma	0.034	0.051	0.098	0.185	0.278
TC_FemSpn2Juv	RickerK	sigma	0.040	0.065	0.111	0.171	0.227

Table D 4: Percentiles of posterior distributions for autocorrelation parameters (phi)

DataSet	Model	Parameter	p10	p25	p50	p75	p90
TC_Spn2Ad	**RickerAR1**	**phi**	**0.497**	**0.595**	**0.702**	**0.789**	**0.855**
TC_Spn2AdAlt	RickerAR1	phi	0.325	0.430	0.537	0.642	0.729
TC_Spn2Juv	RickerAR1	phi	0.376	0.512	0.671	0.795	0.875
TC_FemSpn2Ad	RickerAR1	phi	0.343	0.447	0.546	0.634	0.705
TC_FemSpn2AdAlt	RickerAR1	phi	0.416	0.537	0.656	0.763	0.859
TC_FemSpn2Juv	RickerAR1	phi	0.214	0.349	0.486	0.609	0.711

Table D 5: Percentiles of posterior distributions for Ricker Kalman productivity parameters (alpha) by brood year – Total spawner to adult data sets

DataSet	Model	Parameter	p10	p25	p50	p75	p90
TC_Spn2Ad	RickerK	alpha1987	2.185	2.436	2.854	3.419	4.219
TC_Spn2Ad	RickerK	alpha1988	4.010	4.720	5.319	5.869	6.399
TC_Spn2Ad	RickerK	alpha1989	4.088	4.911	5.688	6.368	7.158
TC_Spn2Ad	RickerK	alpha1990	4.272	5.310	6.429	7.380	8.499
TC_Spn2Ad	RickerK	alpha1991	2.966	3.993	4.825	5.829	6.847
TC_Spn2Ad	RickerK	alpha1992	2.064	2.593	3.050	3.558	4.115
TC_Spn2Ad	RickerK	alpha1993	1.162	1.429	1.800	2.291	2.865
TC_Spn2Ad	RickerK	alpha1994	1.159	1.408	1.756	2.196	2.711
TC_Spn2Ad	RickerK	alpha1995	2.143	2.578	2.893	3.209	3.824
TC_Spn2Ad	RickerK	alpha1996	2.945	3.360	3.700	4.070	4.670
TC_Spn2Ad	RickerK	alpha1997	3.564	4.050	4.485	4.984	5.497
TC_Spn2Ad	RickerK	alpha1998	3.773	4.312	4.894	5.568	6.346
TC_Spn2Ad	RickerK	alpha1999	4.966	5.877	6.839	7.671	8.625
TC_Spn2Ad	RickerK	alpha2000	4.587	5.648	6.627	7.531	8.639
TC_Spn2Ad	RickerK	alpha2001	3.610	4.768	5.845	6.988	8.476
TC_Spn2Ad	RickerK	alpha2002	2.571	4.116	5.461	7.258	9.358
TC_Spn2Ad	RickerK	alpha2003	2.357	3.546	4.649	5.977	7.607
TC_Spn2Ad	RickerK	alpha2004	1.812	2.501	3.169	4.078	5.273
TC_Spn2Ad	RickerK	alpha2005	2.351	3.111	3.890	4.828	5.925
TC_Spn2Ad	RickerK	alpha2006	2.909	3.941	4.919	5.844	6.895
TC_Spn2Ad	RickerK	alpha2007	3.269	4.104	4.991	5.671	6.463
TC_Spn2Ad	RickerK	alpha2008	2.253	2.818	3.323	3.965	4.849
TC_Spn2Ad	RickerK	alpha2009	2.143	2.683	3.165	3.896	4.758
TC_Spn2AdAlt	RickerK	alpha1987	1.995	2.495	3.106	3.728	4.412
TC_Spn2AdAlt	RickerK	alpha1988	3.590	4.261	5.038	5.815	6.666
TC_Spn2AdAlt	RickerK	alpha1989	3.826	4.520	5.454	6.298	7.378
TC_Spn2AdAlt	RickerK	alpha1990	3.774	4.622	5.658	6.770	8.028
TC_Spn2AdAlt	RickerK	alpha1991	2.545	3.500	4.531	5.557	6.783
TC_Spn2AdAlt	RickerK	alpha1992	1.847	2.443	3.125	3.834	4.699
TC_Spn2AdAlt	RickerK	alpha1993	0.988	1.412	1.878	2.598	3.548
TC_Spn2AdAlt	RickerK	alpha1994	1.044	1.513	1.957	2.569	3.525
TC_Spn2AdAlt	RickerK	alpha1995	2.322	2.713	3.272	3.789	4.456
TC_Spn2AdAlt	RickerK	alpha1996	2.948	3.488	4.010	4.646	5.354
TC_Spn2AdAlt	RickerK	alpha1997	3.786	4.325	4.942	5.657	6.321
TC_Spn2AdAlt	RickerK	alpha1998	4.427	5.209	6.324	7.467	8.528
TC_Spn2AdAlt	RickerK	alpha1999	4.315	5.093	6.236	7.350	8.519
TC_Spn2AdAlt	RickerK	alpha2000	4.041	4.777	5.749	6.937	8.152
TC_Spn2AdAlt	RickerK	alpha2001	2.540	3.778	5.025	6.344	7.812
TC_Spn2AdAlt	RickerK	alpha2002	1.716	3.308	5.025	6.990	10.145
TC_Spn2AdAlt	RickerK	alpha2003	1.805	3.101	4.401	5.974	8.335
TC_Spn2AdAlt	RickerK	alpha2004	1.712	2.625	3.575	4.776	6.349
TC_Spn2AdAlt	RickerK	alpha2005	1.659	2.623	3.519	4.660	6.042
TC_Spn2AdAlt	RickerK	alpha2006	2.670	3.625	4.783	6.131	7.932
TC_Spn2AdAlt	RickerK	alpha2007	2.315	2.936	3.620	4.435	5.478
TC_Spn2AdAlt	RickerK	alpha2008	2.035	2.724	3.497	4.383	5.315
TC_Spn2AdAlt	RickerK	alpha2009	1.819	2.420	3.143	4.004	4.993

Table D 6: Percentiles of posterior distributions for Ricker Kalman productivity parameters (alpha) by brood year – Female spawner to adult data sets

DataSet	Model	Parameter	p10	p25	p50	p75	p90
TC_FemSpn2Ad	RickerK	alpha1987	2.356	2.566	2.941	3.445	3.971
TC_FemSpn2Ad	RickerK	alpha1988	4.364	4.985	5.502	6.054	6.644
TC_FemSpn2Ad	RickerK	alpha1989	4.672	5.368	6.008	6.728	7.369
TC_FemSpn2Ad	RickerK	alpha1990	5.336	6.199	7.038	7.958	9.209
TC_FemSpn2Ad	RickerK	alpha1991	3.951	4.476	5.436	6.874	8.197
TC_FemSpn2Ad	RickerK	alpha1992	2.726	3.027	3.370	3.891	4.372
TC_FemSpn2Ad	RickerK	alpha1993	1.377	1.585	1.885	2.287	2.790
TC_FemSpn2Ad	RickerK	alpha1994	1.415	1.600	1.871	2.183	2.591
TC_FemSpn2Ad	RickerK	alpha1995	2.532	2.823	3.143	3.448	3.807
TC_FemSpn2Ad	RickerK	alpha1996	3.263	3.622	3.936	4.343	4.769
TC_FemSpn2Ad	RickerK	alpha1997	3.907	4.285	4.617	5.017	5.482
TC_FemSpn2Ad	RickerK	alpha1998	4.332	4.716	5.222	5.867	6.361
TC_FemSpn2Ad	RickerK	alpha1999	5.750	6.699	7.577	8.488	9.324
TC_FemSpn2Ad	RickerK	alpha2000	5.199	5.876	6.662	7.697	8.647
TC_FemSpn2Ad	RickerK	alpha2001	4.619	5.398	6.305	7.450	8.555
TC_FemSpn2Ad	RickerK	alpha2002	3.942	4.646	5.991	7.858	9.609
TC_FemSpn2Ad	RickerK	alpha2003	3.753	4.554	6.100	8.291	11.571
TC_FemSpn2Ad	RickerK	alpha2004	2.371	2.877	3.550	4.635	5.755
TC_FemSpn2Ad	RickerK	alpha2005	3.056	3.521	4.247	5.260	6.248
TC_FemSpn2Ad	RickerK	alpha2006	3.812	4.487	5.428	6.671	7.967
TC_FemSpn2Ad	RickerK	alpha2007	4.100	4.773	5.473	6.221	6.933
TC_FemSpn2Ad	RickerK	alpha2008	2.670	3.039	3.548	4.190	4.932
TC_FemSpn2Ad	RickerK	alpha2009	2.578	2.892	3.446	4.107	4.717
TC_FemSpn2AdAlt	RickerK	alpha1987	2.179	2.504	2.898	3.546	4.331
TC_FemSpn2AdAlt	RickerK	alpha1988	3.582	4.236	4.852	5.703	6.238
TC_FemSpn2AdAlt	RickerK	alpha1989	4.025	4.667	5.520	6.325	7.083
TC_FemSpn2AdAlt	RickerK	alpha1990	4.147	5.006	6.074	7.143	8.019
TC_FemSpn2AdAlt	RickerK	alpha1991	2.819	3.394	4.452	5.740	6.845
TC_FemSpn2AdAlt	RickerK	alpha1992	2.196	2.595	3.122	3.649	4.254
TC_FemSpn2AdAlt	RickerK	alpha1993	1.118	1.399	1.812	2.327	2.981
TC_FemSpn2AdAlt	RickerK	alpha1994	1.231	1.495	1.863	2.310	3.037
TC_FemSpn2AdAlt	RickerK	alpha1995	2.580	2.910	3.406	3.886	4.389
TC_FemSpn2AdAlt	RickerK	alpha1996	3.211	3.670	4.137	4.587	5.077
TC_FemSpn2AdAlt	RickerK	alpha1997	3.912	4.491	5.061	5.584	6.094
TC_FemSpn2AdAlt	RickerK	alpha1998	4.747	5.560	6.683	7.661	8.491
TC_FemSpn2AdAlt	RickerK	alpha1999	4.529	5.462	6.411	7.415	8.401
TC_FemSpn2AdAlt	RickerK	alpha2000	3.900	4.621	5.390	6.406	7.215
TC_FemSpn2AdAlt	RickerK	alpha2001	3.138	3.713	4.695	5.735	6.932
TC_FemSpn2AdAlt	RickerK	alpha2002	2.567	3.339	4.668	6.158	7.564
TC_FemSpn2AdAlt	RickerK	alpha2003	2.335	3.195	4.593	6.595	8.730
TC_FemSpn2AdAlt	RickerK	alpha2004	2.028	2.623	3.616	4.504	5.801
TC_FemSpn2AdAlt	RickerK	alpha2005	2.027	2.517	3.402	4.230	5.418
TC_FemSpn2AdAlt	RickerK	alpha2006	3.098	3.815	4.766	6.422	7.815
TC_FemSpn2AdAlt	RickerK	alpha2007	2.608	3.062	3.669	4.269	5.023
TC_FemSpn2AdAlt	RickerK	alpha2008	2.297	2.765	3.366	4.128	4.941
TC_FemSpn2AdAlt	RickerK	alpha2009	2.021	2.427	3.070	3.695	4.410

Table D 7: Percentiles of posterior distributions for Ricker Kalman productivity parameters (alpha) by brood year – Juvenile data sets

DataSet	Model	Parameter	p10	p25	p50	p75	p90
TC_Spn2Juv	RickerK	alpha1990	24.576	29.149	34.212	39.533	46.096
TC_Spn2Juv	RickerK	alpha1991	19.684	22.849	26.628	31.674	37.118
TC_Spn2Juv	RickerK	alpha1992	24.295	29.534	35.602	42.571	50.386
TC_Spn2Juv	RickerK	alpha1993	22.170	25.774	30.104	35.186	39.540
TC_Spn2Juv	RickerK	alpha1994	18.343	20.916	24.251	28.196	31.886
TC_Spn2Juv	RickerK	alpha1995	22.049	25.010	28.207	31.530	34.815
TC_Spn2Juv	RickerK	alpha1996	26.750	29.667	32.727	36.003	40.267
TC_Spn2Juv	RickerK	alpha1997	36.744	41.744	47.291	52.020	56.522
TC_Spn2Juv	RickerK	alpha1998	42.439	48.305	55.075	61.587	68.289
TC_Spn2Juv	RickerK	alpha1999	47.392	54.153	61.523	68.739	76.479
TC_Spn2Juv	RickerK	alpha2000	51.233	59.935	69.439	78.504	87.726
TC_Spn2Juv	RickerK	alpha2001	51.247	61.385	73.364	87.914	104.060
TC_Spn2Juv	RickerK	alpha2002	49.536	65.012	86.745	113.423	147.361
TC_Spn2Juv	RickerK	alpha2003	53.758	68.957	92.560	120.728	159.007
TC_Spn2Juv	RickerK	alpha2004	48.109	58.952	73.186	88.153	106.287
TC_Spn2Juv	RickerK	alpha2005	44.245	54.748	66.800	81.144	96.870
TC_Spn2Juv	RickerK	alpha2006	42.472	51.655	62.413	73.728	86.177
TC_Spn2Juv	RickerK	alpha2007	42.514	51.100	60.365	69.977	79.752
TC_Spn2Juv	RickerK	alpha2008	37.591	44.088	51.916	60.907	70.195
TC_Spn2Juv	RickerK	alpha2009	29.748	34.957	41.176	47.925	55.424
TC_Spn2Juv	RickerK	alpha2010	26.899	32.053	38.567	45.853	54.555
TC_FemSpn2Juv	RickerK	alpha1990	24.629	28.913	34.311	40.364	46.510
TC_FemSpn2Juv	RickerK	alpha1991	20.008	23.090	27.517	32.870	40.819
TC_FemSpn2Juv	RickerK	alpha1992	24.415	29.028	34.591	41.605	48.416
TC_FemSpn2Juv	RickerK	alpha1993	21.720	25.069	29.409	34.821	40.954
TC_FemSpn2Juv	RickerK	alpha1994	18.748	21.482	24.490	28.212	32.385
TC_FemSpn2Juv	RickerK	alpha1995	22.957	25.578	28.930	32.600	36.280
TC_FemSpn2Juv	RickerK	alpha1996	27.589	30.457	33.692	37.280	41.178
TC_FemSpn2Juv	RickerK	alpha1997	36.717	41.342	46.880	52.318	57.490
TC_FemSpn2Juv	RickerK	alpha1998	42.777	48.713	55.112	62.997	71.607
TC_FemSpn2Juv	RickerK	alpha1999	46.522	54.536	61.998	70.222	78.854
TC_FemSpn2Juv	RickerK	alpha2000	47.885	55.889	65.054	75.438	85.171
TC_FemSpn2Juv	RickerK	alpha2001	47.683	58.001	70.256	84.805	99.054
TC_FemSpn2Juv	RickerK	alpha2002	46.597	59.740	76.531	97.622	126.891
TC_FemSpn2Juv	RickerK	alpha2003	51.543	68.506	92.786	130.497	193.982
TC_FemSpn2Juv	RickerK	alpha2004	46.504	58.451	73.914	92.869	116.458
TC_FemSpn2Juv	RickerK	alpha2005	43.744	53.524	64.864	81.586	99.528
TC_FemSpn2Juv	RickerK	alpha2006	42.021	50.333	61.190	73.911	88.942
TC_FemSpn2Juv	RickerK	alpha2007	41.943	49.851	59.393	69.605	80.726
TC_FemSpn2Juv	RickerK	alpha2008	36.061	42.518	50.387	59.821	70.038
TC_FemSpn2Juv	RickerK	alpha2009	28.767	33.902	39.872	47.369	56.806
TC_FemSpn2Juv	RickerK	alpha2010	25.777	30.941	37.683	45.845	55.235

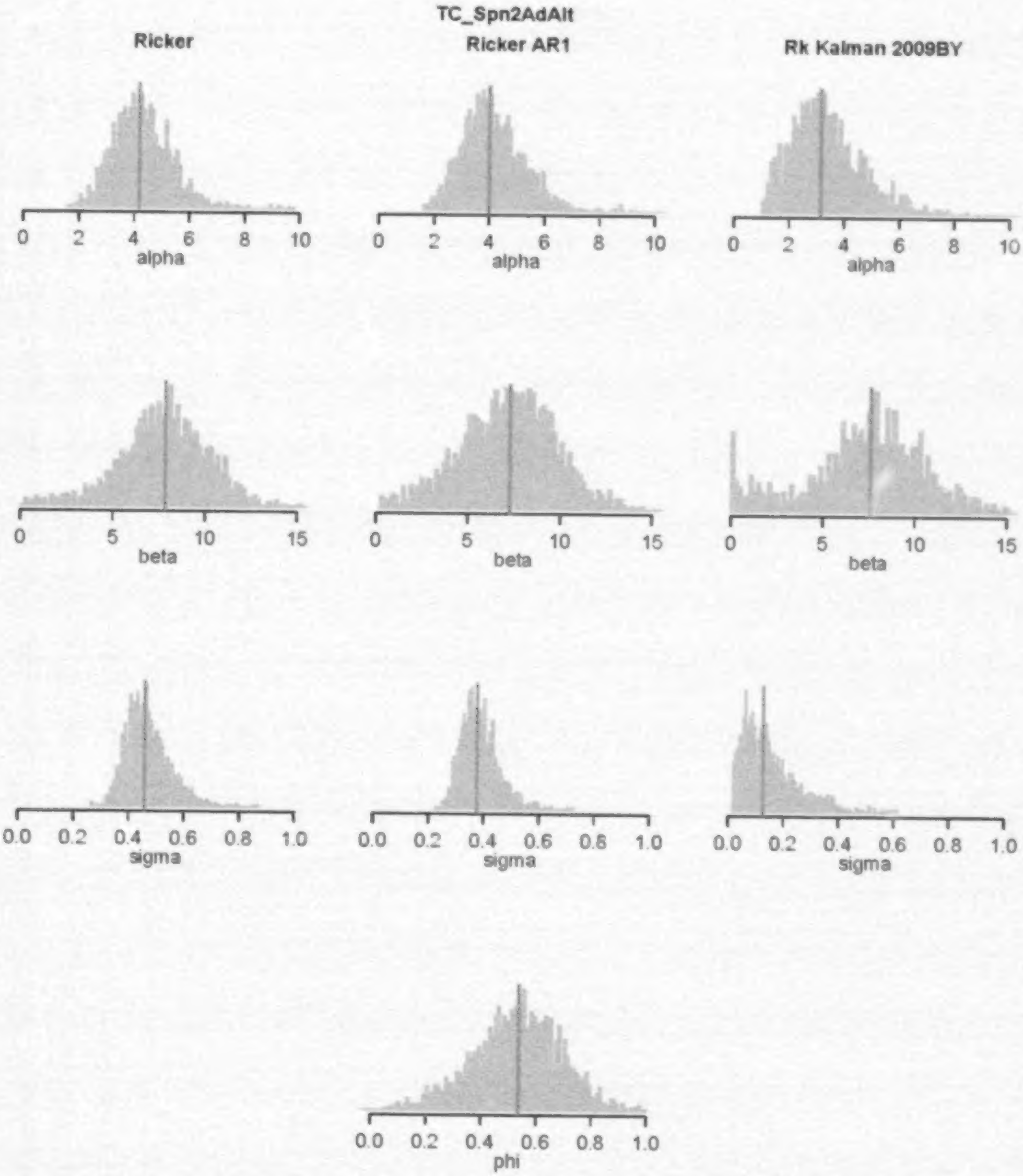


Figure D 1: Posterior distribution of model parameters – Spn2AltAd

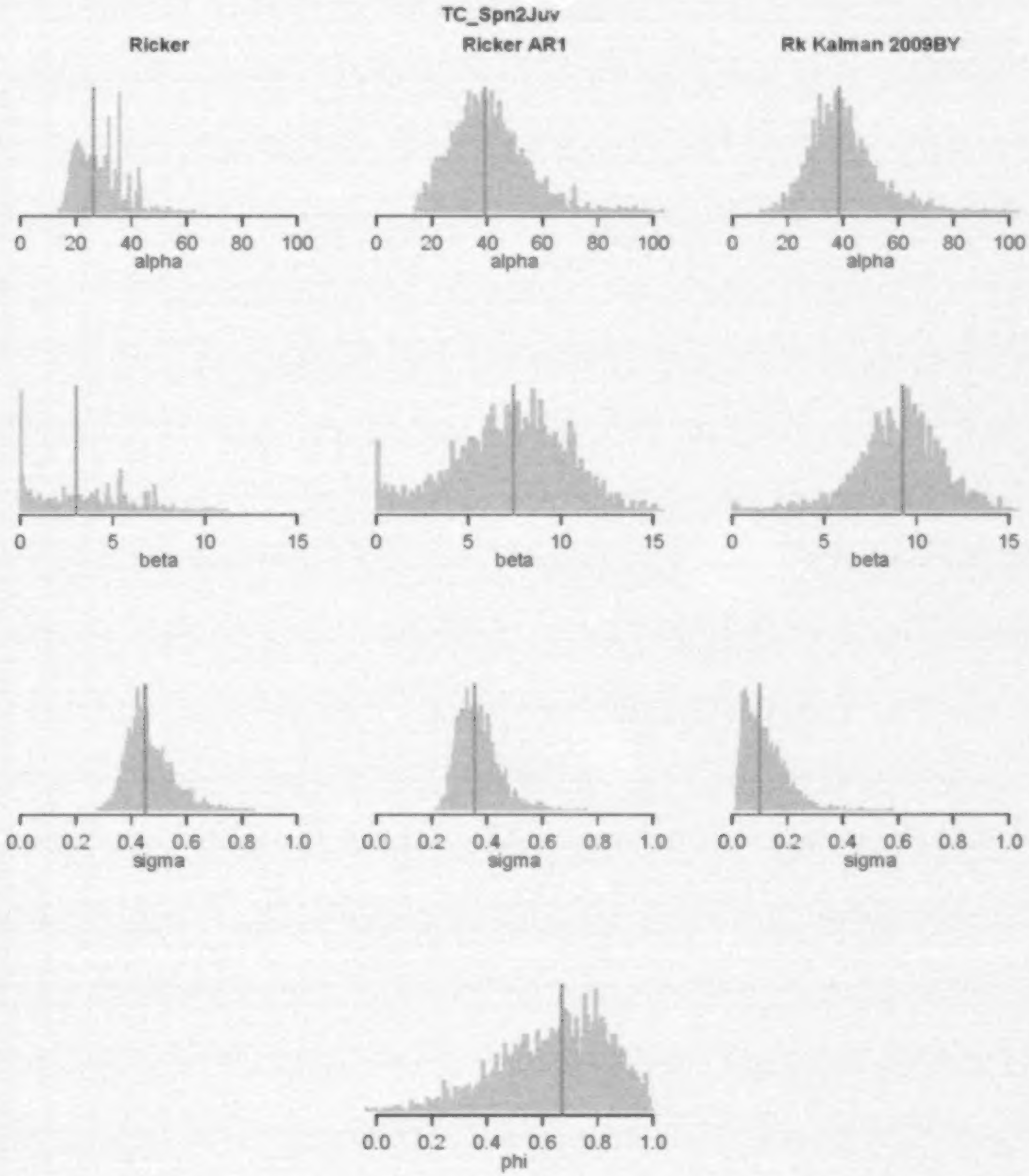


Figure D 2: Posterior distribution of model parameters – Spn2Juv

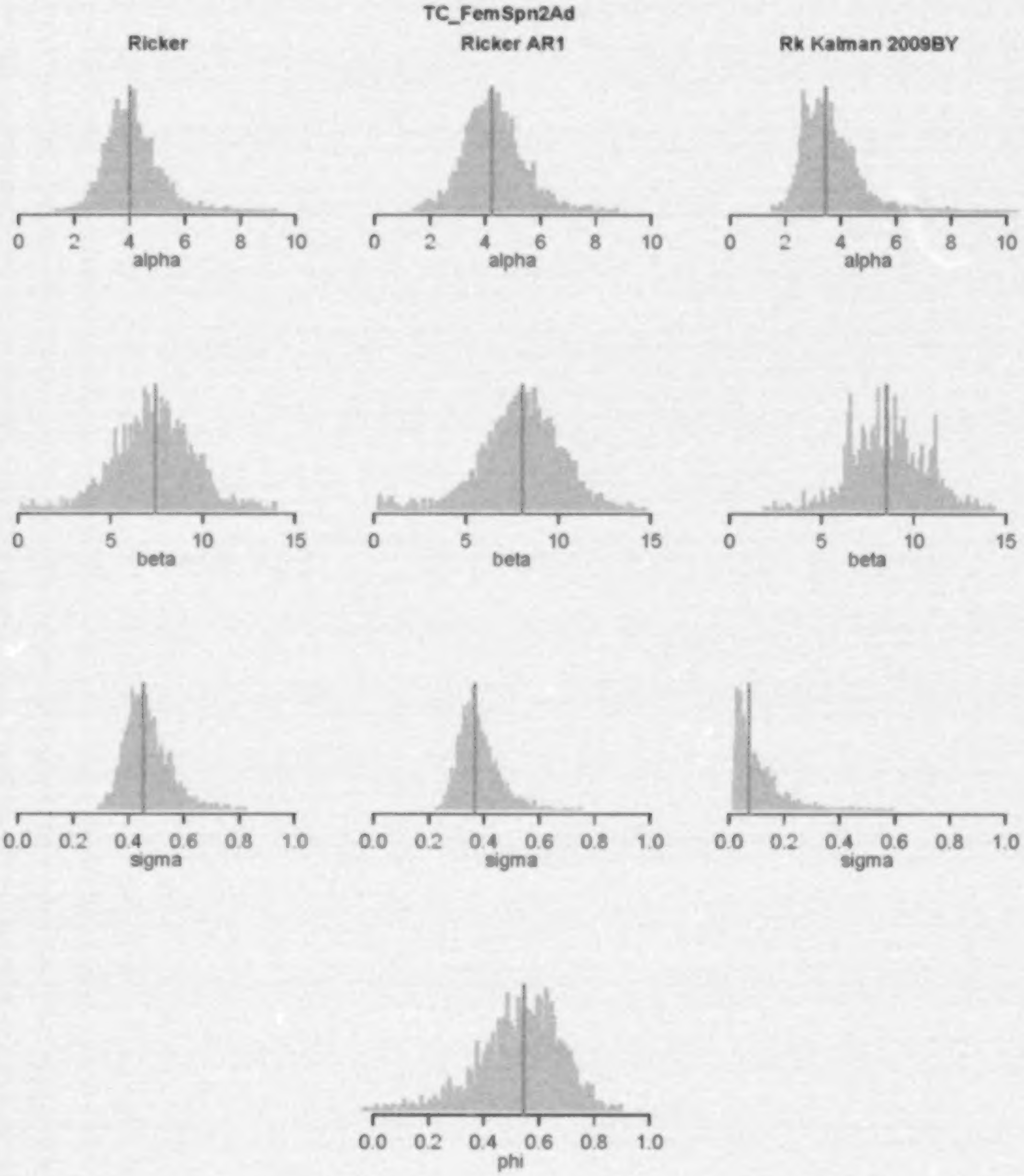


Figure D 3: Posterior distribution of model parameters – FemSpn2Ad

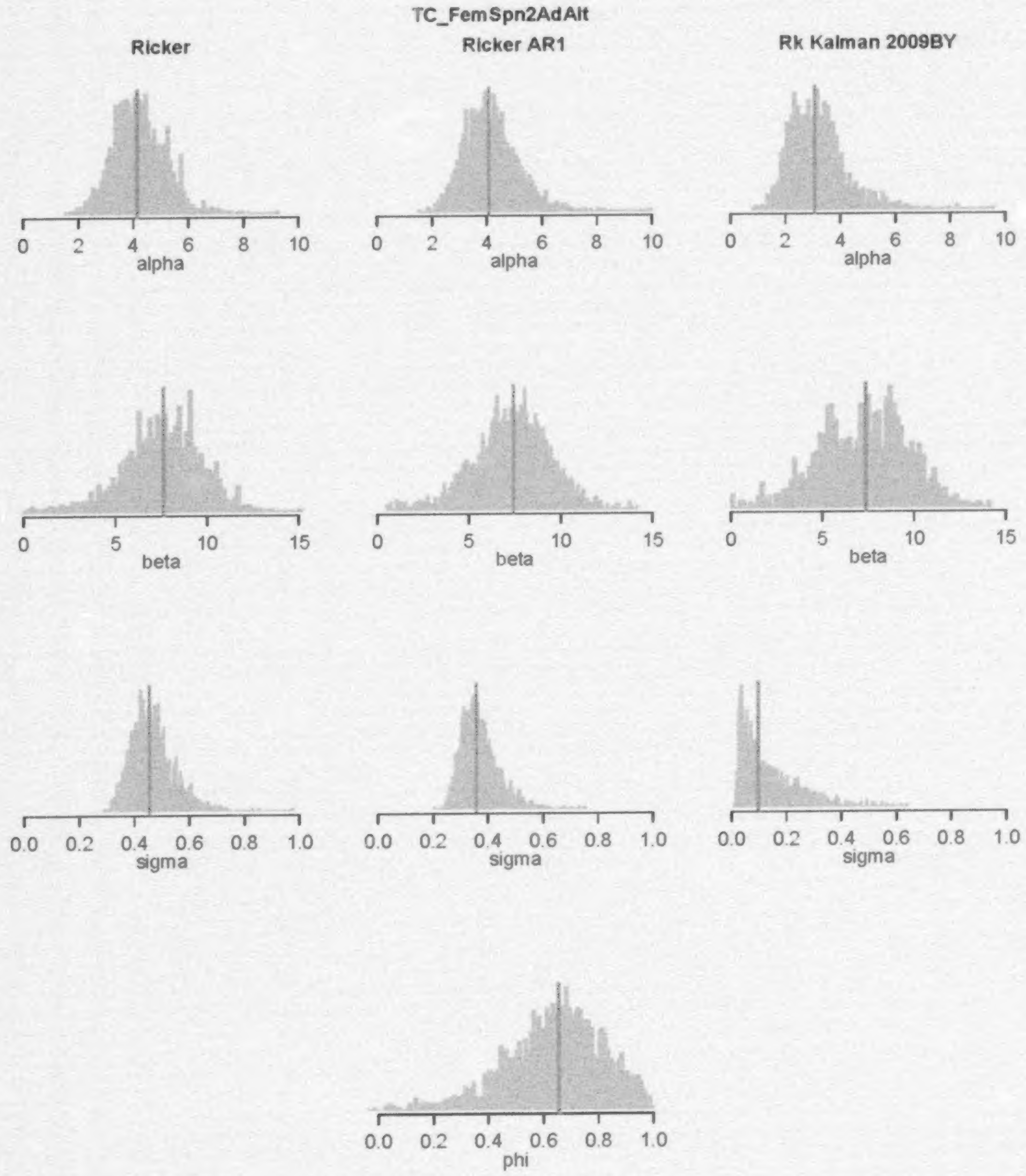


Figure D 4: Posterior distribution of model parameters – FemSpn2AltAd

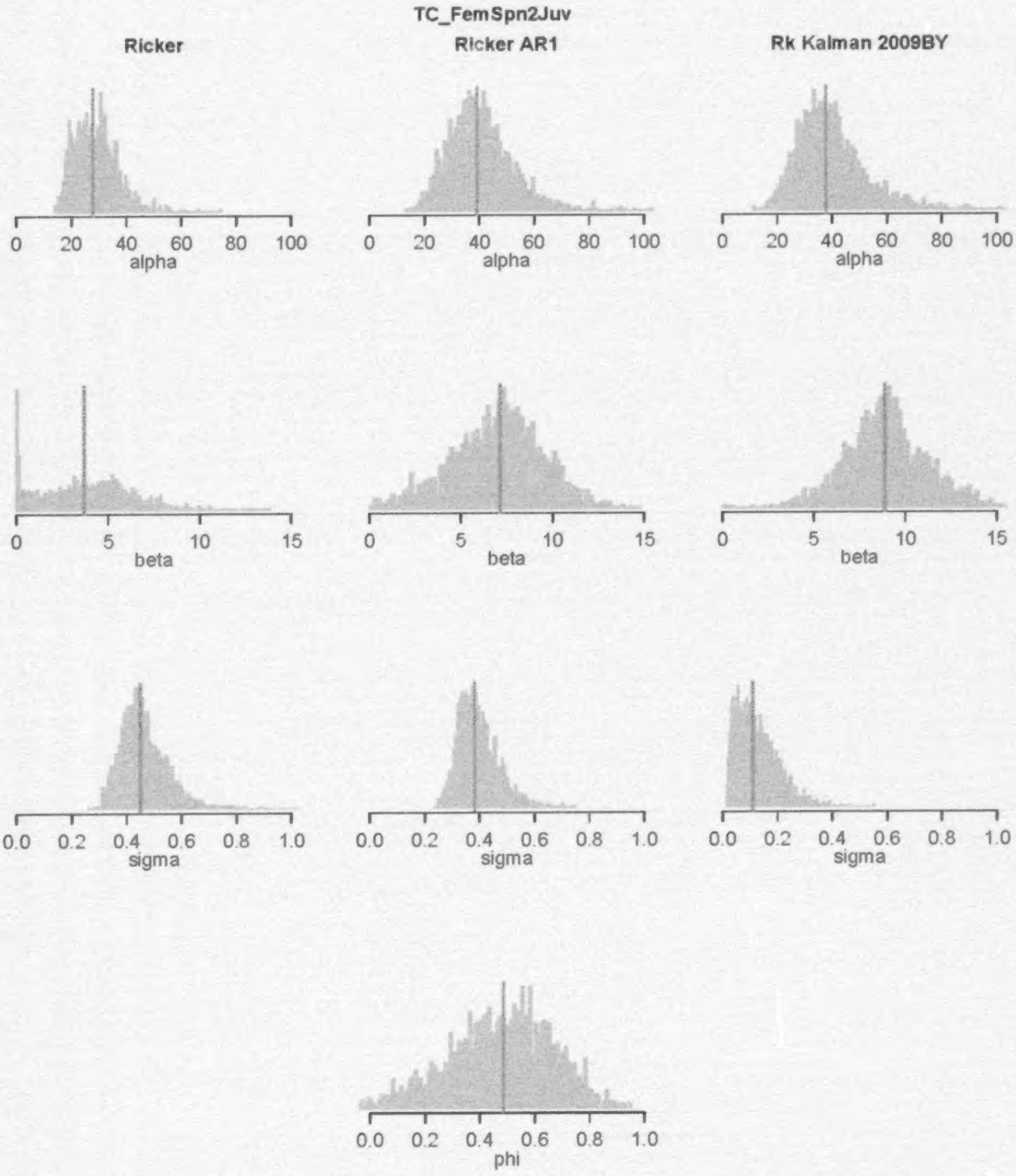


Figure D 5: Posterior distribution of model parameters – FemSpn2Juv

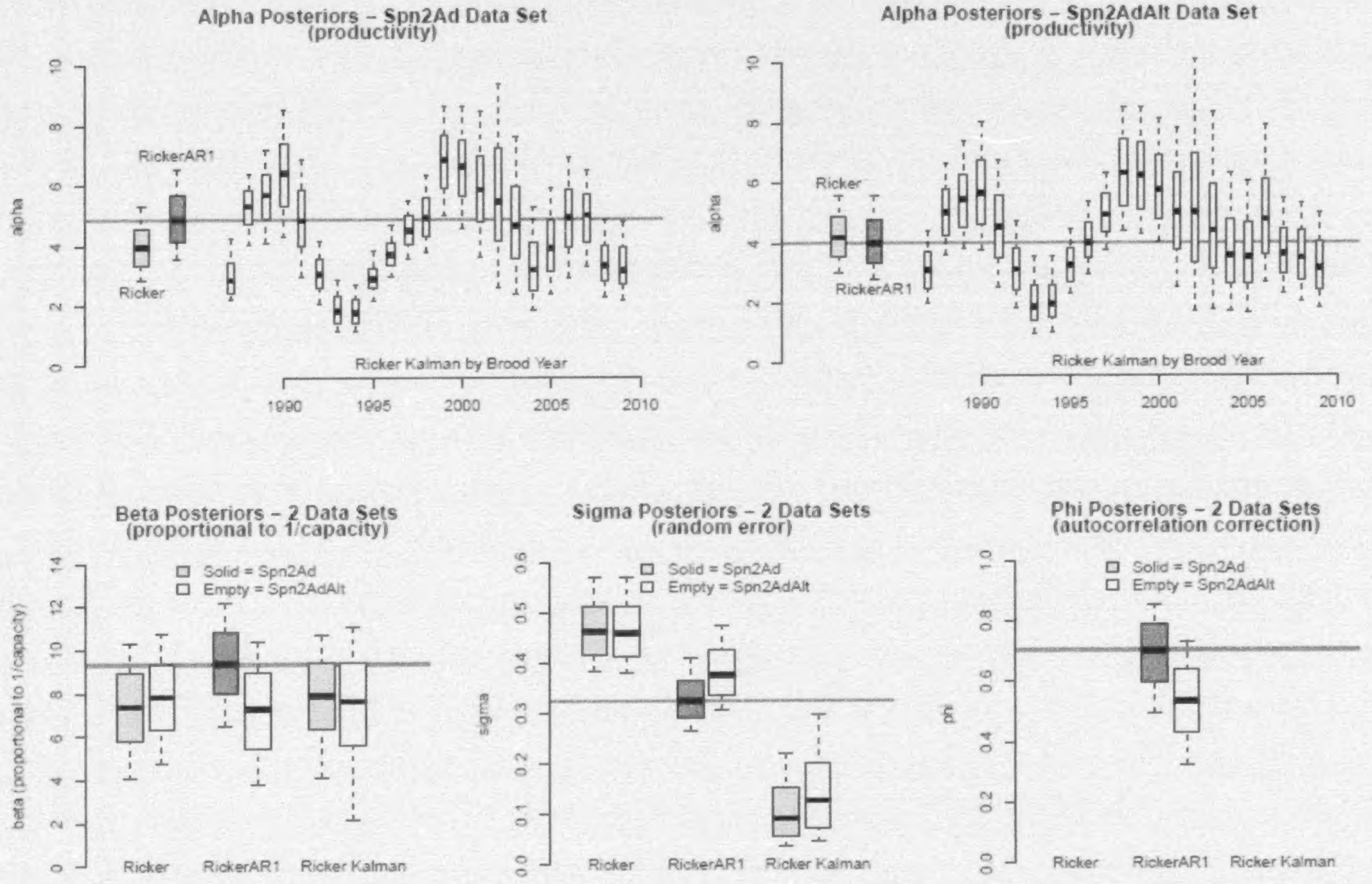


Figure D 6: Posterior distribution of model parameters – Boxplot comparison

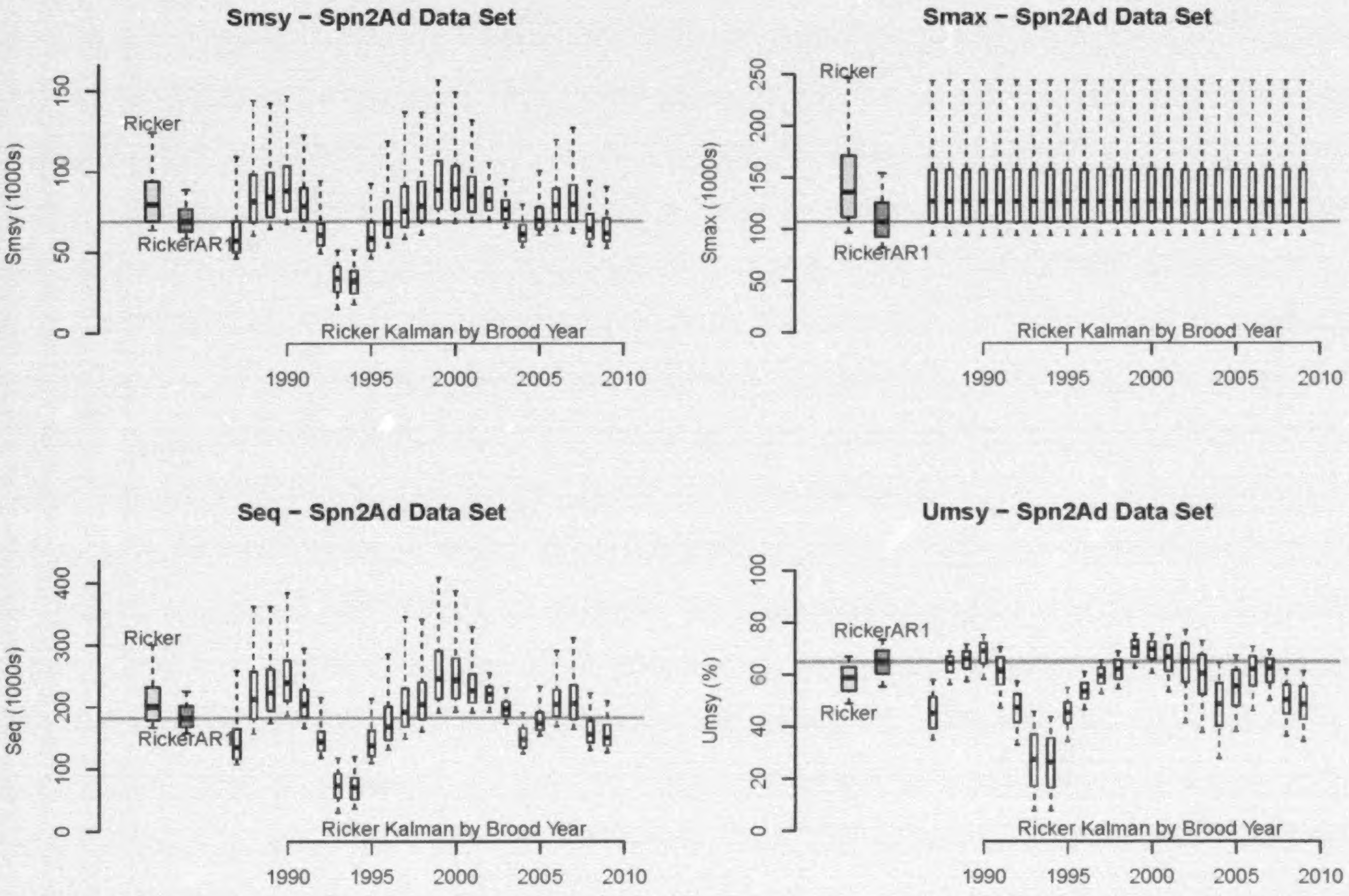


Figure D 7: Posterior distribution of biological benchmarks – Boxplot comparison